

# SEQUENCE LISTING

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<120> POLYPEPTIDE COMPOSITIONS TOXIC TO COLEOPTERAN INSECTS

<130> MECO:218--1 11792.0218.DVUS01

<150> 09/427,770  
 <151> 1999-10-27

<150> 08/993,722  
 <151> 1997-12-18

<160> 113

<170> PatentIn version 3.2

<210> 1  
 <211> 1959  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Recombinant delta endotoxin

<220>  
 <221> CDS  
 <222> (1)..(1956)

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Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp	
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Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala	100	105	110	
caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt				384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser	115	120	125	
aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat				432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr	130	135	140	
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tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa				672
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Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile	290	295	300	

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 <213> Artificial sequence

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Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp 50 55 60
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val 65 70 75 80



Gly	Val	Pro	Phe	Ala	Gly	Ala	Leu	Thr	Ser	Phe	Tyr	Gln	Ser	Phe	Leu	85	90	95
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Gln	Val	Glu	Val	Leu	Ile	Asp	Lys	Lys	Ile	Glu	Glu	Tyr	Ala	Lys	Ser	115	120	125
Lys	Ala	Leu	Ala	Glu	Leu	Gln	Gly	Leu	Gln	Asn	Asn	Phe	Glu	Asp	Tyr	130	135	140
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Leu	Lys	Asp	Ala	Gln	Val	Phe	Gly	Glu	Glu	Trp	Gly	Tyr	Ser	Ser	Glu	210	215	220
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 Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln  
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 Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly  
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 His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr  
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 Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser  
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<210> 3  
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<220>

<221> CDS

<222> (1)..(1956)

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aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat	96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn	
20 25 30	
cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg	144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met	
35 40 45	
act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat	192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp	
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Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val	
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Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu	
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Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala	
100 105 110	
caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt	384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser	
115 120 125	
aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat	432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr	
130 135 140	
gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt	480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser	
145 150 155 160	
aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt	528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser	
165 170 175	
cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg	576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val	
180 185 190	
ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta	624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu	

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gat gtt gct gaa ttc ctt agt aga caa tta aaa ctt aca caa caa tac Asp Val Ala Glu Phe Leu Ser Arg Gln Leu Lys Leu Thr Gln Gln Tyr 225 230 235 240			720
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ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg 355 360 365			1104
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aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val 385 390 395 400			1200
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gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu 465 470 475 480	1440
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act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser 515 520 525	1584
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gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala 545 550 555 560	1680
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ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys 610 615 620	1872
aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile 625 630 635 640	1920
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 <213> Artificial sequence

<220>  
 <223> Recombinant delta endotoxin

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Pro	Asn	Ser	Thr	Leu	Glu	Glu	Leu	Asn	Tyr	Lys	Glu	Phe	Leu	Arg	Met	35	40	45	
Thr	Glu	Asp	Ser	Ser	Thr	Glu	Val	Leu	Asp	Asn	Ser	Thr	Val	Lys	Asp	50	55	60	
Ala	Val	Gly	Thr	Gly	Ile	Ser	Val	Val	Gly	Gln	Ile	Leu	Gly	Val	Val	65	70	75	80
Gly	Val	Pro	Phe	Ala	Gly	Ala	Leu	Thr	Ser	Phe	Tyr	Gln	Ser	Phe	Leu	85	90	95	
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Gln	Val	Glu	Val	Leu	Ile	Asp	Lys	Lys	Ile	Glu	Glu	Tyr	Ala	Lys	Ser	115	120	125	
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Val	Asn	Ala	Leu	Asn	Ser	Trp	Lys	Lys	Thr	Pro	Leu	Ser	Leu	Arg	Ser	145	150	155	160
Lys	Arg	Ser	Gln	Asp	Arg	Ile	Arg	Glu	Leu	Phe	Ser	Gln	Ala	Glu	Ser	165	170	175	
His	Phe	Arg	Asn	Ser	Met	Pro	Ser	Phe	Ala	Val	Ser	Lys	Phe	Glu	Val	180	185	190	
Leu	Phe	Leu	Pro	Thr	Tyr	Ala	Gln	Ala	Ala	Asn	Thr	His	Leu	Leu	Leu	195	200	205	
Leu	Lys	Asp	Ala	Gln	Val	Phe	Gly	Glu	Glu	Trp	Gly	Tyr	Ser	Ser	Glu	210	215	220	
Asp	Val	Ala	Glu	Phe	Leu	Ser	Arg	Gln	Leu	Lys	Leu	Thr	Gln	Gln	Tyr	225	230	235	240

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 Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu  
 260 265 270  
 Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp  
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 Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly  
 435 440 445  
 His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr  
 450 455 460  
 Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu  
 465 470 475 480  
 Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp  
 485 490 495  
 Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile  
 500 505 510  
 Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser  
 515 520 525  
 Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys  
 530 535 540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala  
 545 550 555 560  
 Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr  
 565 570 575  
 Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile  
 580 585 590  
 Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr  
 595 600 605  
 Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys  
 610 615 620  
 Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile  
 625 630 635 640  
 Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu  
 645 650

<210> 5  
 <211> 1959  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Recombinant delta endotoxin

<220>  
 <221> CDS  
 <222> (1)..(1956)

<400> 5  
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 Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro  
 1 5 10 15  
 aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat 96  
 Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn  
 20 25 30  
 cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg 144  
 Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met  
 35 40 45  
 act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat 192  
 Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp  
 50 55 60  
 gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta 240  
 Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val  
 65 70 75 80  
 gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt 288



Gly	Val	Pro	Phe	Ala	Gly	Ala	Leu	Thr	Ser	Phe	Tyr	Gln	Ser	Phe	Leu		
				85					90					95			
aac	act	ata	tgg	cca	agt	gat	gct	gac	cca	tgg	aag	gct	ttt	atg	gca		336
Asn	Thr	Ile	Trp	Pro	Ser	Asp	Ala	Asp	Pro	Trp	Lys	Ala	Phe	Met	Ala		
			100					105					110				
caa	gtt	gaa	gta	ctg	ata	gat	aag	aaa	ata	gag	gag	tat	gct	aaa	agt		384
Gln	Val	Glu	Val	Leu	Ile	Asp	Lys	Lys	Ile	Glu	Glu	Tyr	Ala	Lys	Ser		
		115					120					125					
aaa	gct	ctt	gca	gag	tta	cag	ggt	ctt	caa	aat	aat	ttc	gaa	gat	tat		432
Lys	Ala	Leu	Ala	Glu	Leu	Gln	Gly	Leu	Gln	Asn	Asn	Phe	Glu	Asp	Tyr		
	130					135					140						
gtt	aat	gcg	tta	aat	tcc	tgg	aag	aaa	aca	cct	tta	agt	ttg	cga	agt		480
Val	Asn	Ala	Leu	Asn	Ser	Trp	Lys	Lys	Thr	Pro	Leu	Ser	Leu	Arg	Ser		
145					150					155					160		
aaa	aga	agc	caa	gat	cga	ata	agg	gaa	ctt	ttt	tct	caa	gca	gaa	agt		528
Lys	Arg	Ser	Gln	Asp	Arg	Ile	Arg	Glu	Leu	Phe	Ser	Gln	Ala	Glu	Ser		
				165					170					175			
cat	ttt	cgt	aat	tcc	atg	ccg	tca	ttt	gca	gtt	tcc	aaa	ttc	gaa	gtg		576
His	Phe	Arg	Asn	Ser	Met	Pro	Ser	Phe	Ala	Val	Ser	Lys	Phe	Glu	Val		
			180					185					190				
ctg	ttt	cta	cca	aca	tat	gca	caa	gct	gca	aat	aca	cat	tta	ttg	cta		624
Leu	Phe	Leu	Pro	Thr	Tyr	Ala	Gln	Ala	Ala	Asn	Thr	His	Leu	Leu	Leu		
		195					200					205					
tta	aaa	gat	gct	caa	gtt	ttt	gga	gaa	gaa	tgg	gga	tat	tct	cca	gaa		672
Leu	Lys	Asp	Ala	Gln	Val	Phe	Gly	Glu	Glu	Trp	Gly	Tyr	Ser	Pro	Glu		
	210					215					220						
gat	gtt	gct	gaa	ttc	agt	cat	aga	caa	tta	aaa	ctt	aca	caa	caa	tac		720
Asp	Val	Ala	Glu	Phe	Ser	His	Arg	Gln	Leu	Lys	Leu	Thr	Gln	Gln	Tyr		
225					230				235					240			
act	gac	cat	tgt	gtt	aat	tgg	tat	aat	gtt	gga	tta	aat	ggt	tta	aga		768
Thr	Asp	His	Cys	Val	Asn	Trp	Tyr	Asn	Val	Gly	Leu	Asn	Gly	Leu	Arg		
				245				250					255				
ggt	tca	act	tat	gat	gca	tgg	gtc	aaa	ttt	aac	cgt	ttt	cgc	aga	gaa		816
Gly	Ser	Thr	Tyr	Asp	Ala	Trp	Val	Lys	Phe	Asn	Arg	Phe	Arg	Arg	Glu		
			260				265						270				
atg	act	tta	act	gta	tta	gat	cta	att	gta	ctt	ttc	cca	ttt	tat	gat		864
Met	Thr	Leu	Thr	Val	Leu	Asp	Leu	Ile	Val	Leu	Phe	Pro	Phe	Tyr	Asp		
		275					280					285					
att	cgg	tta	tac	tca	aaa	ggg	gtt	aaa	aca	gaa	cta	aca	aga	gac	att		912
Ile	Arg	Leu	Tyr	Ser	Lys	Gly	Val	Lys	Thr	Glu	Leu	Thr	Arg	Asp	Ile		
	290					295					300						
ttt	acg	gat	cca	att	ttt	tca	ctt	aat	act	ctt	cag	gag	tat	gga	cca		960
Phe	Thr	Asp	Pro	Ile	Phe	Ser	Leu	Asn	Thr	Leu	Gln	Glu	Tyr	Gly	Pro		

305	310	315	320	
act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat				1008
Thr Phe Leu Ser	Ile Glu Asn Ser	Ile Arg Lys Pro	His Leu Phe Asp	
	325	330	335	
tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt				1056
Tyr Leu Gln Gly	Ile Glu Phe His	Thr Arg Leu Gln	Pro Gly Tyr Phe	
	340	345	350	
ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga				1104
Gly Lys Asp Ser	Phe Asn Tyr Trp	Ser Gly Asn Tyr	Val Glu Thr Arg	
	355	360	365	
cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat				1152
Pro Ser Ile Gly	Ser Ser Lys Thr	Ile Thr Ser Pro	Phe Tyr Gly Asp	
	370	375	380	
aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt				1200
Lys Ser Thr Glu	Pro Val Gln Lys	Leu Ser Phe Asp	Gly Gln Lys Val	
	385	390	400	
tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag				1248
Tyr Arg Thr Ile	Ala Asn Thr Asp	Val Ala Ala Trp	Pro Asn Gly Lys	
	405	410	415	
gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa				1296
Val Tyr Leu Gly	Val Thr Lys Val	Asp Phe Ser Gln	Tyr Asp Asp Gln	
	420	425	430	
aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc				1344
Lys Asn Glu Thr	Ser Thr Gln Thr	Tyr Asp Ser Lys	Arg Asn Asn Gly	
	435	440	445	
cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca				1392
His Val Ser Ala	Gln Asp Ser Ile	Asp Gln Leu Pro	Pro Pro Glu Thr Thr	
	450	455	460	
gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa				1440
Asp Glu Pro Leu	Glu Lys Ala Tyr	Ser His Gln Leu	Asn Tyr Ala Glu	
	465	470	480	
tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg				1488
Cys Phe Leu Met	Gln Asp Arg Arg	Gly Thr Ile Pro	Phe Phe Thr Trp	
	485	490	495	
aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att				1536
Thr His Arg Ser	Val Asp Phe Phe	Asn Thr Ile Asp	Ala Glu Lys Ile	
	500	505	510	
act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc				1584
Thr Gln Leu Pro	Val Val Lys Ala	Tyr Ala Leu Ser	Ser Gly Ala Ser	
	515	520	525	
att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa				1632
Ile Ile Glu Gly	Pro Gly Phe Thr	Gly Gly Asn Leu	Leu Leu Phe Leu Lys	
	530	535	540	

gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca	1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala	
545 550 555 560	
gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act	1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr	
565 570 575	
aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc	1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile	
580 585 590	
tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca	1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr	
595 600 605	
ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag	1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys	
610 615 620	
aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc	1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile	
625 630 635 640	
tat ata gat aag ata gaa ttt atc cca gta caa ttg taa	1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu	
645 650	

<210> 6  
 <211> 652  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Recombinant delta endotoxin

<400> 6

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro	
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Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn	
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Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met	
35 40 45	
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp	
50 55 60	
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val	
65 70 75 80	
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu	
85 90 95	

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Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys  
 405 410 415  
 Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln  
 420 425 430  
 Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly  
 435 440 445  
 His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr  
 450 455 460  
 Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu  
 465 470 475 480  
 Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp  
 485 490 495  
 Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile  
 500 505 510  
 Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser  
 515 520 525  
 Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys  
 530 535 540  
 Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala  
 545 550 555 560  
 Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr  
 565 570 575  
 Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile  
 580 585 590  
 Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr  
 595 600 605  
 Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys  
 610 615 620  
 Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile  
 625 630 635 640  
 Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu  
 645 650

<210> 7  
 <211> 1959  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Recombinant delta endotoxin

<220>

<221> CDS

<222> (1)..(1956)

<400> 7

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aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat 96  
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn  
20 25 30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg 144  
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met  
35 40 45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat 192  
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp  
50 55 60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta 240  
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val  
65 70 75 80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt 288  
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu  
85 90 95

aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca 336  
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala  
100 105 110

caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt 384  
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser  
115 120 125

aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat 432  
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr  
130 135 140

gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt 480  
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser  
145 150 155 160

aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt 528  
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser  
165 170 175

cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg 576  
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val  
180 185 190

ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta 624  
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu

195	200	205	
tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu 210 215 220			672
gat gtt gct gaa ttc tat cgt aga caa tta aaa ctt aca caa caa tac Asp Val Ala Glu Phe Tyr Arg Arg Gln Leu Lys Leu Thr Gln Gln Tyr 225 230 235 240			720
act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg 245 250 255			768
ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu 260 265 270			816
atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp 275 280 285			864
att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile 290 295 300			912
ttt acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro 305 310 315 320			960
act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp 325 330 335			1008
tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe 340 345 350			1056
ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg 355 360 365			1104
cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp 370 375 380			1152
aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val 385 390 395 400			1200
tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys 405 410 415			1248
gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln 420 425 430			1296

aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc	1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly	
435 440 445	
cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca	1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr	
450 455 460	
gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa	1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu	
465 470 475 480	
tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg	1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp	
485 490 495	
aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att	1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile	
500 505 510	
act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc	1584
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser	
515 520 525	
att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa	1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys	
530 535 540	
gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca	1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala	
545 550 555 560	
gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act	1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr	
565 570 575	
aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc	1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile	
580 585 590	
tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca	1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr	
595 600 605	
ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag	1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys	
610 615 620	
aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc	1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile	
625 630 635 640	
tat ata gat aag ata gaa ttt atc cca gta caa ttg taa	1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu	
645 650	



<210> 8  
 <211> 652  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Recombinant delta endotoxin

<400> 8

Met	Asn	Pro	Asn	Asn	Arg	Ser	Glu	His	Asp	Thr	Ile	Lys	Val	Thr	Pro	1	5	10	15
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Pro	Asn	Ser	Thr	Leu	Glu	Glu	Leu	Asn	Tyr	Lys	Glu	Phe	Leu	Arg	Met	35	40	45	
Thr	Glu	Asp	Ser	Ser	Thr	Glu	Val	Leu	Asp	Asn	Ser	Thr	Val	Lys	Asp	50	55	60	
Ala	Val	Gly	Thr	Gly	Ile	Ser	Val	Val	Gly	Gln	Ile	Leu	Gly	Val	Val	65	70	75	80
Gly	Val	Pro	Phe	Ala	Gly	Ala	Leu	Thr	Ser	Phe	Tyr	Gln	Ser	Phe	Leu	85	90	95	
Asn	Thr	Ile	Trp	Pro	Ser	Asp	Ala	Asp	Pro	Trp	Lys	Ala	Phe	Met	Ala	100	105	110	
Gln	Val	Glu	Val	Leu	Ile	Asp	Lys	Lys	Ile	Glu	Glu	Tyr	Ala	Lys	Ser	115	120	125	
Lys	Ala	Leu	Ala	Glu	Leu	Gln	Gly	Leu	Gln	Asn	Asn	Phe	Glu	Asp	Tyr	130	135	140	
Val	Asn	Ala	Leu	Asn	Ser	Trp	Lys	Lys	Thr	Pro	Leu	Ser	Leu	Arg	Ser	145	150	155	160
Lys	Arg	Ser	Gln	Asp	Arg	Ile	Arg	Glu	Leu	Phe	Ser	Gln	Ala	Glu	Ser	165	170	175	
His	Phe	Arg	Asn	Ser	Met	Pro	Ser	Phe	Ala	Val	Ser	Lys	Phe	Glu	Val	180	185	190	
Leu	Phe	Leu	Pro	Thr	Tyr	Ala	Gln	Ala	Ala	Asn	Thr	His	Leu	Leu	Leu	195	200	205	
Leu	Lys	Asp	Ala	Gln	Val	Phe	Gly	Glu	Glu	Trp	Gly	Tyr	Ser	Ser	Glu	210	215	220	
Asp	Val	Ala	Glu	Phe	Tyr	Arg	Arg	Gln	Leu	Lys	Leu	Thr	Gln	Gln	Tyr	225	230	235	240
Thr	Asp	His	Cys	Val	Asn	Trp	Tyr	Asn	Val	Gly	Leu	Asn	Gly	Leu	Arg				

245										250					255				
Gly	Ser	Thr	Tyr	Asp	Ala	Trp	Val	Lys	Phe	Asn	Arg	Phe	Arg	Arg	Glu				
			260					265					270						
Met	Thr	Leu	Thr	Val	Leu	Asp	Leu	Ile	Val	Leu	Phe	Pro	Phe	Tyr	Asp				
		275					280					285							
Ile	Arg	Leu	Tyr	Ser	Lys	Gly	Val	Lys	Thr	Glu	Leu	Thr	Arg	Asp	Ile				
	290					295					300								
Phe	Thr	Asp	Pro	Ile	Phe	Ser	Leu	Asn	Thr	Leu	Gln	Glu	Tyr	Gly	Pro				
305					310					315					320				
Thr	Phe	Leu	Ser	Ile	Glu	Asn	Ser	Ile	Arg	Lys	Pro	His	Leu	Phe	Asp				
				325					330						335				
Tyr	Leu	Gln	Gly	Ile	Glu	Phe	His	Thr	Arg	Leu	Gln	Pro	Gly	Tyr	Phe				
			340					345					350						
Gly	Lys	Asp	Ser	Phe	Asn	Tyr	Trp	Ser	Gly	Asn	Tyr	Val	Glu	Thr	Arg				
		355					360					365							
Pro	Ser	Ile	Gly	Ser	Ser	Lys	Thr	Ile	Thr	Ser	Pro	Phe	Tyr	Gly	Asp				
	370					375					380								
Lys	Ser	Thr	Glu	Pro	Val	Gln	Lys	Leu	Ser	Phe	Asp	Gly	Gln	Lys	Val				
385					390					395					400				
Tyr	Arg	Thr	Ile	Ala	Asn	Thr	Asp	Val	Ala	Ala	Trp	Pro	Asn	Gly	Lys				
				405					410					415					
Val	Tyr	Leu	Gly	Val	Thr	Lys	Val	Asp	Phe	Ser	Gln	Tyr	Asp	Asp	Gln				
			420					425					430						
Lys	Asn	Glu	Thr	Ser	Thr	Gln	Thr	Tyr	Asp	Ser	Lys	Arg	Asn	Asn	Gly				
		435					440					445							
His	Val	Ser	Ala	Gln	Asp	Ser	Ile	Asp	Gln	Leu	Pro	Pro	Glu	Thr	Thr				
	450					455					460								
Asp	Glu	Pro	Leu	Glu	Lys	Ala	Tyr	Ser	His	Gln	Leu	Asn	Tyr	Ala	Glu				
465					470					475					480				
Cys	Phe	Leu	Met	Gln	Asp	Arg	Arg	Gly	Thr	Ile	Pro	Phe	Phe	Thr	Trp				
				485				490						495					
Thr	His	Arg	Ser	Val	Asp	Phe	Phe	Asn	Thr	Ile	Asp	Ala	Glu	Lys	Ile				
			500					505					510						
Thr	Gln	Leu	Pro	Val	Val	Lys	Ala	Tyr	Ala	Leu	Ser	Ser	Gly	Ala	Ser				
		515					520					525							
Ile	Ile	Glu	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Asn	Leu	Leu	Phe	Leu	Lys				
	530					535					540								
Glu	Ser	Ser	Asn	Ser	Ile	Ala	Lys	Phe	Lys	Val	Thr	Leu	Asn	Ser	Ala				



85										90					95					
aac	act	ata	tgg	cca	agt	gat	gct	gac	cca	tgg	aag	gct	ttt	atg	gca	336				
Asn	Thr	Ile	Trp	Pro	Ser	Asp	Ala	Asp	Pro	Trp	Lys	Ala	Phe	Met	Ala					
			100					105					110							
caa	gtt	gaa	gta	ctg	ata	gat	aag	aaa	ata	gag	gag	tat	gct	aaa	agt	384				
Gln	Val	Glu	Val	Leu	Ile	Asp	Lys	Lys	Ile	Glu	Glu	Tyr	Ala	Lys	Ser					
		115					120					125								
aaa	gct	ctt	gca	gag	tta	cag	ggg	ctt	caa	aat	aat	ttc	gaa	gat	tat	432				
Lys	Ala	Leu	Ala	Glu	Leu	Gln	Gly	Leu	Gln	Asn	Asn	Phe	Glu	Asp	Tyr					
	130					135					140									
gtt	aat	gcg	tta	aat	tcc	tgg	aag	aaa	aca	cct	tta	agt	ttg	cga	agt	480				
Val	Asn	Ala	Leu	Asn	Ser	Trp	Lys	Lys	Thr	Pro	Leu	Ser	Leu	Arg	Ser					
145					150					155					160					
aaa	aga	agc	caa	gat	cga	ata	agg	gaa	ctt	ttt	tct	caa	gca	gaa	agt	528				
Lys	Arg	Ser	Gln	Asp	Arg	Ile	Arg	Glu	Leu	Phe	Ser	Gln	Ala	Glu	Ser					
			165					170						175						
cat	ttt	cgt	aat	tcc	atg	ccg	tca	ttt	gca	gtt	tcc	aaa	ttc	gaa	gtg	576				
His	Phe	Arg	Asn	Ser	Met	Pro	Ser	Phe	Ala	Val	Ser	Lys	Phe	Glu	Val					
			180					185					190							
ctg	ttt	cta	cca	aca	tat	gca	caa	gct	gca	aat	aca	cat	tta	ttg	cta	624				
Leu	Phe	Leu	Pro	Thr	Tyr	Ala	Gln	Ala	Ala	Asn	Thr	His	Leu	Leu	Leu					
		195					200					205								
tta	aaa	gat	gct	caa	gtt	ttt	gga	gaa	gaa	tgg	gga	tat	tct	tca	gaa	672				
Leu	Lys	Asp	Ala	Gln	Val	Phe	Gly	Glu	Glu	Trp	Gly	Tyr	Ser	Ser	Glu					
	210					215					220									
gat	gtt	gct	gaa	ttc	tat	aat	aga	caa	tta	aaa	ctt	aca	caa	caa	tac	720				
Asp	Val	Ala	Glu	Phe	Tyr	Asn	Arg	Gln	Leu	Lys	Leu	Thr	Gln	Gln	Tyr					
225					230					235					240					
tct	gac	cat	tgt	gtt	aat	tgg	tat	aat	gtt	gga	tta	aat	ggg	tta	aga	768				
Ser	Asp	His	Cys	Val	Asn	Trp	Tyr	Asn	Val	Gly	Leu	Asn	Gly	Leu	Arg					
			245					250						255						
ggg	tca	act	tat	gat	gca	tgg	gtc	aaa	ttt	aac	cgt	ttt	cgc	aga	gaa	816				
Gly	Ser	Thr	Tyr	Asp	Ala	Trp	Val	Lys	Phe	Asn	Arg	Phe	Arg	Arg	Glu					
			260					265					270							
atg	act	tta	act	gta	tta	gat	cta	att	gta	ctt	ttc	cca	ttt	tat	gat	864				
Met	Thr	Leu	Thr	Val	Leu	Asp	Leu	Ile	Val	Leu	Phe	Pro	Phe	Tyr	Asp					
		275					280					285								
att	cgg	tta	tac	tca	aaa	ggg	gtt	aaa	aca	gaa	cta	aca	aga	gac	att	912				
Ile	Arg	Leu	Tyr	Ser	Lys	Gly	Val	Lys	Thr	Glu	Leu	Thr	Arg	Asp	Ile					
	290					295					300									
ttt	acg	gat	cca	att	ttt	tca	ctt	aat	act	ctt	cag	gag	tat	gga	cca	960				
Phe	Thr	Asp	Pro	Ile	Phe	Ser	Leu	Asn	Thr	Leu	Gln	Glu	Tyr	Gly	Pro					
305					310					315					320					

act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp 325 330 335	1008
tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe 340 345 350	1056
ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg 355 360 365	1104
cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp 370 375 380	1152
aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val 385 390 395 400	1200
tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys 405 410 415	1248
gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln 420 425 430	1296
aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly 435 440 445	1344
cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr 450 455 460	1392
gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu 465 470 475 480	1440
tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp 485 490 495	1488
aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile 500 505 510	1536
act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser 515 520 525	1584
att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys 530 535 540	1632

gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca	1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala	
545 550 555 560	
gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act	1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr	
565 570 575	
aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc	1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile	
580 585 590	
tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca	1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr	
595 600 605	
ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag	1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys	
610 615 620	
aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc	1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile	
625 630 635 640	
tat ata gat aag ata gaa ttt atc cca gta caa ttg taa	1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu	
645 650	

<210> 10  
 <211> 652  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Recombinant delta endotoxin

<400> 10

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Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn	
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Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met	
35 40 45	
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp	
50 55 60	
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val	
65 70 75 80	
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu	
85 90 95	

Asn	Thr	Ile	Trp	Pro	Ser	Asp	Ala	Asp	Pro	Trp	Lys	Ala	Phe	Met	Ala		
			100					105						110			
Gln	Val	Glu	Val	Leu	Ile	Asp	Lys	Lys	Ile	Glu	Glu	Tyr	Ala	Lys	Ser		
		115					120					125					
Lys	Ala	Leu	Ala	Glu	Leu	Gln	Gly	Leu	Gln	Asn	Asn	Phe	Glu	Asp	Tyr		
	130					135					140						
Val	Asn	Ala	Leu	Asn	Ser	Trp	Lys	Lys	Thr	Pro	Leu	Ser	Leu	Arg	Ser		
145					150					155					160		
Lys	Arg	Ser	Gln	Asp	Arg	Ile	Arg	Glu	Leu	Phe	Ser	Gln	Ala	Glu	Ser		
				165					170						175		
His	Phe	Arg	Asn	Ser	Met	Pro	Ser	Phe	Ala	Val	Ser	Lys	Phe	Glu	Val		
			180					185						190			
Leu	Phe	Leu	Pro	Thr	Tyr	Ala	Gln	Ala	Ala	Asn	Thr	His	Leu	Leu	Leu		
		195					200					205					
Leu	Lys	Asp	Ala	Gln	Val	Phe	Gly	Glu	Glu	Trp	Gly	Tyr	Ser	Ser	Glu		
	210					215					220						
Asp	Val	Ala	Glu	Phe	Tyr	Asn	Arg	Gln	Leu	Lys	Leu	Thr	Gln	Gln	Tyr		
225					230					235					240		
Ser	Asp	His	Cys	Val	Asn	Trp	Tyr	Asn	Val	Gly	Leu	Asn	Gly	Leu	Arg		
				245					250					255			
Gly	Ser	Thr	Tyr	Asp	Ala	Trp	Val	Lys	Phe	Asn	Arg	Phe	Arg	Arg	Glu		
			260					265					270				
Met	Thr	Leu	Thr	Val	Leu	Asp	Leu	Ile	Val	Leu	Phe	Pro	Phe	Tyr	Asp		
		275					280					285					
Ile	Arg	Leu	Tyr	Ser	Lys	Gly	Val	Lys	Thr	Glu	Leu	Thr	Arg	Asp	Ile		
	290					295					300						
Phe	Thr	Asp	Pro	Ile	Phe	Ser	Leu	Asn	Thr	Leu	Gln	Glu	Tyr	Gly	Pro		
305					310					315					320		
Thr	Phe	Leu	Ser	Ile	Glu	Asn	Ser	Ile	Arg	Lys	Pro	His	Leu	Phe	Asp		
				325					330					335			
Tyr	Leu	Gln	Gly	Ile	Glu	Phe	His	Thr	Arg	Leu	Gln	Pro	Gly	Tyr	Phe		
			340					345					350				
Gly	Lys	Asp	Ser	Phe	Asn	Tyr	Trp	Ser	Gly	Asn	Tyr	Val	Glu	Thr	Arg		
		355					360					365					
Pro	Ser	Ile	Gly	Ser	Ser	Lys	Thr	Ile	Thr	Ser	Pro	Phe	Tyr	Gly	Asp		
	370					375					380						
Lys	Ser	Thr	Glu	Pro	Val	Gln	Lys	Leu	Ser	Phe	Asp	Gly	Gln	Lys	Val		
385					390					395					400		

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys  
 405 410 415  
 Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln  
 420 425 430  
 Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly  
 435 440 445  
 His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr  
 450 455 460  
 Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu  
 465 470 475 480  
 Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp  
 485 490 495  
 Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile  
 500 505 510  
 Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser  
 515 520 525  
 Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys  
 530 535 540  
 Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala  
 545 550 555 560  
 Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr  
 565 570 575  
 Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile  
 580 585 590  
 Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr  
 595 600 605  
 Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys  
 610 615 620  
 Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile  
 625 630 635 640  
 Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu  
 645 650

<210> 11

<211> 1959

<212> DNA

<213> Artificial sequence

<220>

<223> Recombinant delta endotoxin



<220>

<221> CDS

<222> (1)..(1956)

<400> 11

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1 5 10 15

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat 96  
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn  
20 25 30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg 144  
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met  
35 40 45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat 192  
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp  
50 55 60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta 240  
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val  
65 70 75 80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt 288  
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu  
85 90 95

aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca 336  
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala  
100 105 110

caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt 384  
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser  
115 120 125

aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat 432  
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr  
130 135 140

gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt 480  
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser  
145 150 155 160

aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt 528  
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser  
165 170 175

cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg 576  
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val  
180 185 190

ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta 624  
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu  
195 200 205

tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu 210 215 220	672
gat gtt gct gaa ttc tat acc aga caa tta aaa ctt aca caa caa tac Asp Val Ala Glu Phe Tyr Thr Arg Gln Leu Lys Leu Thr Gln Gln Tyr 225 230 235 240	720
act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg 245 250 255	768
ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu 260 265 270	816
atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp 275 280 285	864
att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile 290 295 300	912
ttt acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro 305 310 315 320	960
act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp 325 330 335	1008
tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe 340 345 350	1056
ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg 355 360 365	1104
cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp 370 375 380	1152
aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val 385 390 395 400	1200
tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys 405 410 415	1248
gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln 420 425 430	1296

aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly 435 440 445	1344
cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr 450 455 460	1392
gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu 465 470 475 480	1440
tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp 485 490 495	1488
aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile 500 505 510	1536
act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser 515 520 525	1584
att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys 530 535 540	1632
gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala 545 550 555 560	1680
gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr 565 570 575	1728
aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile 580 585 590	1776
tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr 595 600 605	1824
ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys 610 615 620	1872
aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile 625 630 635 640	1920
tat ata gat aag ata gaa ttt atc cca gta caa ttg taa Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu 645 650	1959

<210> 12  
 <211> 652  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Recombinant delta endotoxin

<400> 12

Met	Asn	Pro	Asn	Asn	Arg	Ser	Glu	His	Asp	Thr	Ile	Lys	Val	Thr	Pro	1	5	10	15
Asn	Ser	Glu	Leu	Gln	Thr	Asn	His	Asn	Gln	Tyr	Pro	Leu	Ala	Asp	Asn	20	25	30	
Pro	Asn	Ser	Thr	Leu	Glu	Glu	Leu	Asn	Tyr	Lys	Glu	Phe	Leu	Arg	Met	35	40	45	
Thr	Glu	Asp	Ser	Ser	Thr	Glu	Val	Leu	Asp	Asn	Ser	Thr	Val	Lys	Asp	50	55	60	
Ala	Val	Gly	Thr	Gly	Ile	Ser	Val	Val	Gly	Gln	Ile	Leu	Gly	Val	Val	65	70	75	80
Gly	Val	Pro	Phe	Ala	Gly	Ala	Leu	Thr	Ser	Phe	Tyr	Gln	Ser	Phe	Leu	85	90	95	
Asn	Thr	Ile	Trp	Pro	Ser	Asp	Ala	Asp	Pro	Trp	Lys	Ala	Phe	Met	Ala	100	105	110	
Gln	Val	Glu	Val	Leu	Ile	Asp	Lys	Lys	Ile	Glu	Glu	Tyr	Ala	Lys	Ser	115	120	125	
Lys	Ala	Leu	Ala	Glu	Leu	Gln	Gly	Leu	Gln	Asn	Asn	Phe	Glu	Asp	Tyr	130	135	140	
Val	Asn	Ala	Leu	Asn	Ser	Trp	Lys	Lys	Thr	Pro	Leu	Ser	Leu	Arg	Ser	145	150	155	160
Lys	Arg	Ser	Gln	Asp	Arg	Ile	Arg	Glu	Leu	Phe	Ser	Gln	Ala	Glu	Ser	165	170	175	
His	Phe	Arg	Asn	Ser	Met	Pro	Ser	Phe	Ala	Val	Ser	Lys	Phe	Glu	Val	180	185	190	
Leu	Phe	Leu	Pro	Thr	Tyr	Ala	Gln	Ala	Ala	Asn	Thr	His	Leu	Leu	Leu	195	200	205	
Leu	Lys	Asp	Ala	Gln	Val	Phe	Gly	Glu	Glu	Trp	Gly	Tyr	Ser	Ser	Glu	210	215	220	
Asp	Val	Ala	Glu	Phe	Tyr	Thr	Arg	Gln	Leu	Lys	Leu	Thr	Gln	Gln	Tyr	225	230	235	240
Thr	Asp	His	Cys	Val	Asn	Trp	Tyr	Asn	Val	Gly	Leu	Asn	Gly	Leu	Arg	245	250	255	

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu  
 260 265 270  
 Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp  
 275 280 285  
 Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile  
 290 295 300  
 Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro  
 305 310 315 320  
 Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp  
 325 330 335  
 Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe  
 340 345 350  
 Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg  
 355 360 365  
 Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp  
 370 375 380  
 Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val  
 385 390 395 400  
 Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys  
 405 410 415  
 Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln  
 420 425 430  
 Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly  
 435 440 445  
 His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr  
 450 455 460  
 Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu  
 465 470 475 480  
 Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp  
 485 490 495  
 Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile  
 500 505 510  
 Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser  
 515 520 525  
 Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys  
 530 535 540  
 Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala  
 545 550 555 560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr  
565 570 575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile  
580 585 590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr  
595 600 605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys  
610 615 620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile  
625 630 635 640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu  
645 650

<210> 13  
<211> 1959  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Recombinant delta endotoxin

<220>  
<221> CDS  
<222> (1)..(1956)

<400> 13  
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Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro  
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aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat 96  
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn  
20 25 30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg 144  
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met  
35 40 45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat 192  
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp  
50 55 60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta 240  
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val  
65 70 75 80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt 288  
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu  
85 90 95

aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala 100 105 110	336
caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser 115 120 125	384
aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr 130 135 140	432
gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser 145 150 155 160	480
aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser 165 170 175	528
cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val 180 185 190	576
ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu 195 200 205	624
tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu 210 215 220	672
gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr 225 230 235 240	720
act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg 245 250 255	768
ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu 260 265 270	816
atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp 275 280 285	864
att aat tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att Ile Asn Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile 290 295 300	912
ttt acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro 305 310 315 320	960

act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat	1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp	
325 330 335	
tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt	1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe	
340 345 350	
ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga	1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg	
355 360 365	
cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat	1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp	
370 375 380	
aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt	1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val	
385 390 395 400	
tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag	1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys	
405 410 415	
gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa	1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln	
420 425 430	
aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc	1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly	
435 440 445	
cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca	1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr	
450 455 460	
gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa	1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu	
465 470 475 480	
tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg	1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp	
485 490 495	
aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att	1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile	
500 505 510	
act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc	1584
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser	
515 520 525	
att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa	1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys	
530 535 540	
gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca	1680



Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala	
545 550 555 560	
gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act	1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr	
565 570 575	
aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc	1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile	
580 585 590	
tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca	1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr	
595 600 605	
ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag	1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys	
610 615 620	
aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc	1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile	
625 630 635 640	
tat ata gat aag ata gaa ttt atc cca gta caa ttg taa	1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu	
645 650	

<210> 14  
 <211> 652  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Recombinant delta endotoxin

<400> 14

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Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn	
20 25 30	
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met	
35 40 45	
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp	
50 55 60	
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val	
65 70 75 80	
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu	
85 90 95	
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala	

100					105					110					
Gln	Val	Glu	Val	Leu	Ile	Asp	Lys	Lys	Ile	Glu	Glu	Tyr	Ala	Lys	Ser
		115					120					125			
Lys	Ala	Leu	Ala	Glu	Leu	Gln	Gly	Leu	Gln	Asn	Asn	Phe	Glu	Asp	Tyr
	130					135					140				
Val	Asn	Ala	Leu	Asn	Ser	Trp	Lys	Lys	Thr	Pro	Leu	Ser	Leu	Arg	Ser
145					150					155					160
Lys	Arg	Ser	Gln	Asp	Arg	Ile	Arg	Glu	Leu	Phe	Ser	Gln	Ala	Glu	Ser
				165					170					175	
His	Phe	Arg	Asn	Ser	Met	Pro	Ser	Phe	Ala	Val	Ser	Lys	Phe	Glu	Val
			180					185					190		
Leu	Phe	Leu	Pro	Thr	Tyr	Ala	Gln	Ala	Ala	Asn	Thr	His	Leu	Leu	Leu
		195					200					205			
Leu	Lys	Asp	Ala	Gln	Val	Phe	Gly	Glu	Glu	Trp	Gly	Tyr	Ser	Ser	Glu
	210					215					220				
Asp	Val	Ala	Glu	Phe	Tyr	His	Arg	Gln	Leu	Lys	Leu	Thr	Gln	Gln	Tyr
225					230					235					240
Thr	Asp	His	Cys	Val	Asn	Trp	Tyr	Asn	Val	Gly	Leu	Asn	Gly	Leu	Arg
				245					250					255	
Gly	Ser	Thr	Tyr	Asp	Ala	Trp	Val	Lys	Phe	Asn	Arg	Phe	Arg	Arg	Glu
			260					265					270		
Met	Thr	Leu	Thr	Val	Leu	Asp	Leu	Ile	Val	Leu	Phe	Pro	Phe	Tyr	Asp
		275					280					285			
Ile	Asn	Leu	Tyr	Ser	Lys	Gly	Val	Lys	Thr	Glu	Leu	Thr	Arg	Asp	Ile
	290					295					300				
Phe	Thr	Asp	Pro	Ile	Phe	Ser	Leu	Asn	Thr	Leu	Gln	Glu	Tyr	Gly	Pro
305					310					315					320
Thr	Phe	Leu	Ser	Ile	Glu	Asn	Ser	Ile	Arg	Lys	Pro	His	Leu	Phe	Asp
				325					330					335	
Tyr	Leu	Gln	Gly	Ile	Glu	Phe	His	Thr	Arg	Leu	Gln	Pro	Gly	Tyr	Phe
			340					345					350		
Gly	Lys	Asp	Ser	Phe	Asn	Tyr	Trp	Ser	Gly	Asn	Tyr	Val	Glu	Thr	Arg
		355					360					365			
Pro	Ser	Ile	Gly	Ser	Ser	Lys	Thr	Ile	Thr	Ser	Pro	Phe	Tyr	Gly	Asp
		370				375					380				
Lys	Ser	Thr	Glu	Pro	Val	Gln	Lys	Leu	Ser	Phe	Asp	Gly	Gln	Lys	Val
385					390					395					400
Tyr	Arg	Thr	Ile	Ala	Asn	Thr	Asp	Val	Ala	Ala	Trp	Pro	Asn	Gly	Lys

405					410					415					
Val	Tyr	Leu	Gly	Val	Thr	Lys	Val	Asp	Phe	Ser	Gln	Tyr	Asp	Asp	Gln
			420					425					430		
Lys	Asn	Glu	Thr	Ser	Thr	Gln	Thr	Tyr	Asp	Ser	Lys	Arg	Asn	Asn	Gly
		435					440					445			
His	Val	Ser	Ala	Gln	Asp	Ser	Ile	Asp	Gln	Leu	Pro	Pro	Glu	Thr	Thr
	450					455					460				
Asp	Glu	Pro	Leu	Glu	Lys	Ala	Tyr	Ser	His	Gln	Leu	Asn	Tyr	Ala	Glu
465					470					475					480
Cys	Phe	Leu	Met	Gln	Asp	Arg	Arg	Gly	Thr	Ile	Pro	Phe	Phe	Thr	Trp
				485					490					495	
Thr	His	Arg	Ser	Val	Asp	Phe	Phe	Asn	Thr	Ile	Asp	Ala	Glu	Lys	Ile
			500					505					510		
Thr	Gln	Leu	Pro	Val	Val	Lys	Ala	Tyr	Ala	Leu	Ser	Ser	Gly	Ala	Ser
		515					520					525			
Ile	Ile	Glu	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Asn	Leu	Leu	Phe	Leu	Lys
	530					535					540				
Glu	Ser	Ser	Asn	Ser	Ile	Ala	Lys	Phe	Lys	Val	Thr	Leu	Asn	Ser	Ala
545					550					555					560
Ala	Leu	Leu	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg	Tyr	Ala	Ser	Thr	Thr
				565					570					575	
Asn	Leu	Arg	Leu	Phe	Val	Gln	Asn	Ser	Asn	Asn	Asp	Phe	Leu	Val	Ile
			580					585					590		
Tyr	Ile	Asn	Lys	Thr	Met	Asn	Lys	Asp	Asp	Asp	Leu	Thr	Tyr	Gln	Thr
		595					600					605			
Phe	Asp	Leu	Ala	Thr	Thr	Asn	Ser	Asn	Met	Gly	Phe	Ser	Gly	Asp	Lys
	610					615					620				
Asn	Glu	Leu	Ile	Ile	Gly	Ala	Glu	Ser	Phe	Val	Ser	Asn	Glu	Lys	Ile
625					630					635					640
Tyr	Ile	Asp	Lys	Ile	Glu	Phe	Ile	Pro	Val	Gln	Leu				
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<210> 15

<211> 1959

<212> DNA

<213> Artificial sequence

<220>

<223> Recombinant delta endotoxin

<220>

<221> CDS

<222> (1)..(1956)

<400> 15

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aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat	96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn	
20 25 30	

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg	144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met	
35 40 45	

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat	192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp	
50 55 60	

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta	240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val	
65 70 75 80	

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt	288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu	
85 90 95	

aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca	336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala	
100 105 110	

caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt	384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser	
115 120 125	

aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat	432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr	
130 135 140	

gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt	480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser	
145 150 155 160	

aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt	528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser	
165 170 175	

cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg	576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val	
180 185 190	

ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta	624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu	
195 200 205	

tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu 210 215 220	672
gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr 225 230 235 240	720
act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg 245 250 255	768
ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu 260 265 270	816
atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp 275 280 285	864
att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile 290 295 300	912
ttt acg gat cca att ttt tta ctt act acg ctt cag aag tac gga cca Phe Thr Asp Pro Ile Phe Leu Leu Thr Thr Leu Gln Lys Tyr Gly Pro 305 310 315 320	960
act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp 325 330 335	1008
tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe 340 345 350	1056
ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg 355 360 365	1104
cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp 370 375 380	1152
aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val 385 390 395 400	1200
tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys 405 410 415	1248
gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln 420 425 430	1296
aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc	1344

Lys	Asn	Glu	Thr	Ser	Thr	Gln	Thr	Tyr	Asp	Ser	Lys	Arg	Asn	Asn	Gly		
	435						440					445					
cat	gta	agt	gca	cag	gat	tct	att	gac	caa	tta	ccg	cca	gaa	aca	aca		1392
His	Val	Ser	Ala	Gln	Asp	Ser	Ile	Asp	Gln	Leu	Pro	Pro	Glu	Thr	Thr		
	450					455					460						
gat	gaa	cca	ctt	gaa	aaa	gca	tat	agt	cat	cag	ctt	aat	tac	gcg	gaa		1440
Asp	Glu	Pro	Leu	Glu	Lys	Ala	Tyr	Ser	His	Gln	Leu	Asn	Tyr	Ala	Glu		
	465				470					475					480		
tgt	ttc	tta	atg	cag	gac	cgt	cgt	gga	aca	att	cca	ttt	ttt	act	tgg		1488
Cys	Phe	Leu	Met	Gln	Asp	Arg	Arg	Gly	Thr	Ile	Pro	Phe	Phe	Thr	Trp		
				485				490						495			
aca	cat	aga	agt	gta	gac	ttt	ttt	aat	aca	att	gat	gct	gaa	aag	att		1536
Thr	His	Arg	Ser	Val	Asp	Phe	Phe	Asn	Thr	Ile	Asp	Ala	Glu	Lys	Ile		
			500					505					510				
act	caa	ctt	cca	gta	gtg	aaa	gca	tat	gcc	ttg	tct	tca	ggg	gct	tcc		1584
Thr	Gln	Leu	Pro	Val	Val	Lys	Ala	Tyr	Ala	Leu	Ser	Ser	Gly	Ala	Ser		
		515					520					525					
att	att	gaa	ggg	cca	gga	ttc	aca	gga	gga	aat	tta	cta	ttc	cta	aaa		1632
Ile	Ile	Glu	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Asn	Leu	Leu	Phe	Leu	Lys		
	530					535					540						
gaa	tct	agt	aat	tca	att	gct	aaa	ttt	aaa	gtt	aca	tta	aat	tca	gca		1680
Glu	Ser	Ser	Asn	Ser	Ile	Ala	Lys	Phe	Lys	Val	Thr	Leu	Asn	Ser	Ala		
	545				550					555					560		
gcc	ttg	tta	caa	cga	tat	cgt	gta	aga	ata	cgc	tat	gct	tct	acc	act		1728
Ala	Leu	Leu	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg	Tyr	Ala	Ser	Thr	Thr		
				565					570					575			
aac	tta	cga	ctt	ttt	gtg	caa	aat	tca	aac	aat	gat	ttt	ctt	gtc	atc		1776
Asn	Leu	Arg	Leu	Phe	Val	Gln	Asn	Ser	Asn	Asn	Asp	Phe	Leu	Val	Ile		
			580					585					590				
tac	att	aat	aaa	act	atg	aat	aaa	gat	gat	gat	tta	aca	tat	caa	aca		1824
Tyr	Ile	Asn	Lys	Thr	Met	Asn	Lys	Asp	Asp	Asp	Leu	Thr	Tyr	Gln	Thr		
		595					600					605					
ttt	gat	ctc	gca	act	act	aat	tct	aat	atg	ggg	ttc	tcg	ggg	gat	aag		1872
Phe	Asp	Leu	Ala	Thr	Thr	Asn	Ser	Asn	Met	Gly	Phe	Ser	Gly	Asp	Lys		
	610					615					620						
aat	gaa	ctt	ata	ata	gga	gca	gaa	tct	ttc	gtt	tct	aat	gaa	aaa	atc		1920
Asn	Glu	Leu	Ile	Ile	Gly	Ala	Glu	Ser	Phe	Val	Ser	Asn	Glu	Lys	Ile		
	625				630					635					640		
tat	ata	gat	aag	ata	gaa	ttt	atc	cca	gta	caa	ttg	taa					1959
Tyr	Ile	Asp	Lys	Ile	Glu	Phe	Ile	Pro	Val	Gln	Leu						
				645					650								

<210> 16

<211> 652  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Recombinant delta endotoxin

<400> 16

Met	Asn	Pro	Asn	Asn	Arg	Ser	Glu	His	Asp	Thr	Ile	Lys	Val	Thr	Pro	1	5	10	15
Asn	Ser	Glu	Leu	Gln	Thr	Asn	His	Asn	Gln	Tyr	Pro	Leu	Ala	Asp	Asn	20	25	30	
Pro	Asn	Ser	Thr	Leu	Glu	Glu	Leu	Asn	Tyr	Lys	Glu	Phe	Leu	Arg	Met	35	40	45	
Thr	Glu	Asp	Ser	Ser	Thr	Glu	Val	Leu	Asp	Asn	Ser	Thr	Val	Lys	Asp	50	55	60	
Ala	Val	Gly	Thr	Gly	Ile	Ser	Val	Val	Gly	Gln	Ile	Leu	Gly	Val	Val	65	70	75	80
Gly	Val	Pro	Phe	Ala	Gly	Ala	Leu	Thr	Ser	Phe	Tyr	Gln	Ser	Phe	Leu	85	90	95	
Asn	Thr	Ile	Trp	Pro	Ser	Asp	Ala	Asp	Pro	Trp	Lys	Ala	Phe	Met	Ala	100	105	110	
Gln	Val	Glu	Val	Leu	Ile	Asp	Lys	Lys	Ile	Glu	Glu	Tyr	Ala	Lys	Ser	115	120	125	
Lys	Ala	Leu	Ala	Glu	Leu	Gln	Gly	Leu	Gln	Asn	Asn	Phe	Glu	Asp	Tyr	130	135	140	
Val	Asn	Ala	Leu	Asn	Ser	Trp	Lys	Lys	Thr	Pro	Leu	Ser	Leu	Arg	Ser	145	150	155	160
Lys	Arg	Ser	Gln	Asp	Arg	Ile	Arg	Glu	Leu	Phe	Ser	Gln	Ala	Glu	Ser	165	170	175	
His	Phe	Arg	Asn	Ser	Met	Pro	Ser	Phe	Ala	Val	Ser	Lys	Phe	Glu	Val	180	185	190	
Leu	Phe	Leu	Pro	Thr	Tyr	Ala	Gln	Ala	Ala	Asn	Thr	His	Leu	Leu	Leu	195	200	205	
Leu	Lys	Asp	Ala	Gln	Val	Phe	Gly	Glu	Glu	Trp	Gly	Tyr	Ser	Ser	Glu	210	215	220	
Asp	Val	Ala	Glu	Phe	Tyr	His	Arg	Gln	Leu	Lys	Leu	Thr	Gln	Gln	Tyr	225	230	235	240
Thr	Asp	His	Cys	Val	Asn	Trp	Tyr	Asn	Val	Gly	Leu	Asn	Gly	Leu	Arg	245	250	255	

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu  
 260 265 270  
 Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp  
 275 280 285  
 Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile  
 290 295 300  
 Phe Thr Asp Pro Ile Phe Leu Leu Thr Thr Leu Gln Lys Tyr Gly Pro  
 305 310 315 320  
 Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp  
 325 330 335  
 Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe  
 340 345 350  
 Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg  
 355 360 365  
 Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp  
 370 375 380  
 Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val  
 385 390 395 400  
 Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys  
 405 410 415  
 Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln  
 420 425 430  
 Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly  
 435 440 445  
 His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr  
 450 455 460  
 Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu  
 465 470 475 480  
 Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp  
 485 490 495  
 Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile  
 500 505 510  
 Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser  
 515 520 525  
 Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys  
 530 535 540  
 Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala  
 545 550 555 560



Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr  
565 570 575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile  
580 585 590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr  
595 600 605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys  
610 615 620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile  
625 630 635 640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu  
645 650

<210> 17  
<211> 1959  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Recombinant delta endotoxin

<220>  
<221> CDS  
<222> (1)..(1956)

<400> 17  
atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct 48  
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro  
1 5 10 15

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat 96  
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn  
20 25 30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg 144  
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met  
35 40 45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat 192  
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp  
50 55 60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta 240  
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val  
65 70 75 80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt 288  
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu  
85 90 95

aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca	336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala	
100 105 110	
caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt	384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser	
115 120 125	
aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat	432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr	
130 135 140	
gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt	480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser	
145 150 155 160	
aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt	528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser	
165 170 175	
cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg	576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val	
180 185 190	
ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta	624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu	
195 200 205	
tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa	672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu	
210 215 220	
gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac	720
Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr	
225 230 235 240	
act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga	768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg	
245 250 255	
ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa	816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu	
260 265 270	
atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat	864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp	
275 280 285	
att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att	912
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile	
290 295 300	
ttt acg gat cca att ttt acc ctt aat aca cta cag aag tgc gga cca	960
Phe Thr Asp Pro Ile Phe Thr Leu Asn Thr Leu Gln Lys Cys Gly Pro	
305 310 315 320	
act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat	1008

Thr	Phe	Leu	Ser	Ile	Glu	Asn	Ser	Ile	Arg	Lys	Pro	His	Leu	Phe	Asp	
				325					330					335		
tat	tta	cag	ggg	att	gaa	ttt	cat	acg	cgt	ctt	caa	cct	ggt	tac	ttt	1056
Tyr	Leu	Gln	Gly	Ile	Glu	Phe	His	Thr	Arg	Leu	Gln	Pro	Gly	Tyr	Phe	
			340					345					350			
ggg	aaa	gat	tct	ttc	aat	tat	tgg	tct	ggt	aat	tat	gta	gaa	act	aga	1104
Gly	Lys	Asp	Ser	Phe	Asn	Tyr	Trp	Ser	Gly	Asn	Tyr	Val	Glu	Thr	Arg	
		355					360					365				
cct	agt	ata	gga	tct	agt	aag	aca	att	act	tcc	cca	ttt	tat	gga	gat	1152
Pro	Ser	Ile	Gly	Ser	Ser	Lys	Thr	Ile	Thr	Ser	Pro	Phe	Tyr	Gly	Asp	
	370					375					380					
aaa	tct	act	gaa	cct	gta	caa	aag	cta	agc	ttt	gat	gga	caa	aaa	gtt	1200
Lys	Ser	Thr	Glu	Pro	Val	Gln	Lys	Leu	Ser	Phe	Asp	Gly	Gln	Lys	Val	
385				390					395						400	
tat	cga	act	ata	gct	aat	aca	gac	gta	gcg	gct	tgg	ccg	aat	ggt	aag	1248
Tyr	Arg	Thr	Ile	Ala	Asn	Thr	Asp	Val	Ala	Ala	Trp	Pro	Asn	Gly	Lys	
			405					410						415		
gta	tat	tta	ggt	gtt	acg	aaa	gtt	gat	ttt	agt	caa	tat	gat	gat	caa	1296
Val	Tyr	Leu	Gly	Val	Thr	Lys	Val	Asp	Phe	Ser	Gln	Tyr	Asp	Asp	Gln	
		420					425					430				
aaa	aat	gaa	act	agt	aca	caa	aca	tat	gat	tca	aaa	aga	aac	aat	ggc	1344
Lys	Asn	Glu	Thr	Ser	Thr	Gln	Thr	Tyr	Asp	Ser	Lys	Arg	Asn	Asn	Gly	
		435				440						445				
cat	gta	agt	gca	cag	gat	tct	att	gac	caa	tta	ccg	cca	gaa	aca	aca	1392
His	Val	Ser	Ala	Gln	Asp	Ser	Ile	Asp	Gln	Leu	Pro	Pro	Glu	Thr	Thr	
	450				455						460					
gat	gaa	cca	ctt	gaa	aaa	gca	tat	agt	cat	cag	ctt	aat	tac	gcg	gaa	1440
Asp	Glu	Pro	Leu	Glu	Lys	Ala	Tyr	Ser	His	Gln	Leu	Asn	Tyr	Ala	Glu	
465				470					475					480		
tgt	ttc	tta	atg	cag	gac	cgt	cgt	gga	aca	att	cca	ttt	ttt	act	tgg	1488
Cys	Phe	Leu	Met	Gln	Asp	Arg	Arg	Gly	Thr	Ile	Pro	Phe	Phe	Thr	Trp	
			485					490						495		
aca	cat	aga	agt	gta	gac	ttt	ttt	aat	aca	att	gat	gct	gaa	aag	att	1536
Thr	His	Arg	Ser	Val	Asp	Phe	Phe	Asn	Thr	Ile	Asp	Ala	Glu	Lys	Ile	
			500					505				510				
act	caa	ctt	cca	gta	gtg	aaa	gca	tat	gcc	ttg	tct	tca	ggt	gct	tcc	1584
Thr	Gln	Leu	Pro	Val	Val	Lys	Ala	Tyr	Ala	Leu	Ser	Ser	Gly	Ala	Ser	
		515				520						525				
att	att	gaa	ggt	cca	gga	ttc	aca	gga	gga	aat	tta	cta	ttc	cta	aaa	1632
Ile	Ile	Glu	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Asn	Leu	Leu	Phe	Leu	Lys	
	530					535					540					
gaa	tct	agt	aat	tca	att	gct	aaa	ttt	aaa	gtt	aca	tta	aat	tca	gca	1680
Glu	Ser	Ser	Asn	Ser	Ile	Ala	Lys	Phe	Lys	Val	Thr	Leu	Asn	Ser	Ala	

545	550	555	560	
gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act				1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr	565	570	575	
aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc				1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile	580	585	590	
tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca				1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr	595	600	605	
ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag				1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys	610	615	620	
aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc				1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile	625	630	635	640
tat ata gat aag ata gaa ttt atc cca gta caa ttg taa				1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu	645	650		

<210> 18  
 <211> 652  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Recombinant delta endotoxin

<400> 18

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro				
1	5	10	15	
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn				
20	25	30		
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met				
35	40	45		
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp				
50	55	60		
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val				
65	70	75	80	
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu				
85	90	95		
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala				
100	105	110		

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser  
 115 120 125  
 Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr  
 130 135 140  
 Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser  
 145 150 155 160  
 Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser  
 165 170 175  
 His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val  
 180 185 190  
 Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu  
 195 200 205  
 Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu  
 210 215 220  
 Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr  
 225 230 235 240  
 Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg  
 245 250 255  
 Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu  
 260 265 270  
 Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp  
 275 280 285  
 Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile  
 290 295 300  
 Phe Thr Asp Pro Ile Phe Thr Leu Asn Thr Leu Gln Lys Cys Gly Pro  
 305 310 315 320  
 Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp  
 325 330 335  
 Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe  
 340 345 350  
 Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg  
 355 360 365  
 Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp  
 370 375 380  
 Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val  
 385 390 395 400  
 Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys  
 405 410 415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln  
 420 425 430  
 Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly  
 435 440 445  
 His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr  
 450 455 460  
 Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu  
 465 470 475 480  
 Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp  
 485 490 495  
 Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile  
 500 505 510  
 Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser  
 515 520 525  
 Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys  
 530 535 540  
 Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala  
 545 550 555 560  
 Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr  
 565 570 575  
 Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile  
 580 585 590  
 Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr  
 595 600 605  
 Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys  
 610 615 620  
 Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile  
 625 630 635 640  
 Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu  
 645 650

<210> 19  
 <211> 1959  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Recombinant delta endotoxin

<220>

<221> CDS

<222> (1)..(1956)

<400> 19

atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct	48
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro	
1 5 10 15	

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat	96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn	
20 25 30	

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg	144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met	
35 40 45	

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat	192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp	
50 55 60	

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta	240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val	
65 70 75 80	

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt	288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu	
85 90 95	

aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca	336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala	
100 105 110	

caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt	384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser	
115 120 125	

aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat	432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr	
130 135 140	

gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt	480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser	
145 150 155 160	

aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt	528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser	
165 170 175	

cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg	576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val	
180 185 190	

ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta	624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu	
195 200 205	

tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa	672
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Leu	Lys	Asp	Ala	Gln	Val	Phe	Gly	Glu	Glu	Trp	Gly	Tyr	Ser	Ser	Glu		
210						215					220						
gat	ggt	gct	gaa	ttt	tat	cat	aga	caa	tta	aaa	ctt	aca	caa	caa	tac	720	
Asp	Val	Ala	Glu	Phe	Tyr	His	Arg	Gln	Leu	Lys	Leu	Thr	Gln	Gln	Tyr		
225					230					235					240		
act	gac	cat	tgt	gtt	aat	tgg	tat	aat	gtt	gga	tta	aat	ggt	tta	aga	768	
Thr	Asp	His	Cys	Val	Asn	Trp	Tyr	Asn	Val	Gly	Leu	Asn	Gly	Leu	Arg		
				245					250					255			
ggt	tca	act	tat	gat	gca	tgg	gtc	aaa	ttt	aac	cgt	ttt	cgc	aga	gaa	816	
Gly	Ser	Thr	Tyr	Asp	Ala	Trp	Val	Lys	Phe	Asn	Arg	Phe	Arg	Arg	Glu		
			260					265					270				
atg	act	tta	act	gta	tta	gat	cta	att	gta	ctt	ttc	cca	ttt	tat	gat	864	
Met	Thr	Leu	Thr	Val	Leu	Asp	Leu	Ile	Val	Leu	Phe	Pro	Phe	Tyr	Asp		
		275					280					285					
att	cgg	tta	tac	tca	aaa	ggg	gtt	aaa	aca	gaa	cta	aca	aga	gac	att	912	
Ile	Arg	Leu	Tyr	Ser	Lys	Gly	Val	Lys	Thr	Glu	Leu	Thr	Arg	Asp	Ile		
	290					295					300						
ttt	acg	gat	cca	att	ttt	gcc	gtt	aat	act	ctg	tgg	gaa	tac	gga	cca	960	
Phe	Thr	Asp	Pro	Ile	Phe	Ala	Val	Asn	Thr	Leu	Trp	Glu	Tyr	Gly	Pro		
305					310					315					320		
act	ttt	ttg	agt	ata	gaa	aac	tct	att	cga	aaa	cct	cat	tta	ttt	gat	1008	
Thr	Phe	Leu	Ser	Ile	Glu	Asn	Ser	Ile	Arg	Lys	Pro	His	Leu	Phe	Asp		
				325					330					335			
tat	tta	cag	ggg	att	gaa	ttt	cat	acg	cgt	ctt	caa	cct	ggt	tac	ttt	1056	
Tyr	Leu	Gln	Gly	Ile	Glu	Phe	His	Thr	Arg	Leu	Gln	Pro	Gly	Tyr	Phe		
			340					345					350				
ggg	aaa	gat	tct	ttc	aat	tat	tgg	tct	ggt	aat	tat	gta	gaa	act	aga	1104	
Gly	Lys	Asp	Ser	Phe	Asn	Tyr	Trp	Ser	Gly	Asn	Tyr	Val	Glu	Thr	Arg		
		355					360					365					
cct	agt	ata	gga	tct	agt	aag	aca	att	act	tcc	cca	ttt	tat	gga	gat	1152	
Pro	Ser	Ile	Gly	Ser	Ser	Lys	Thr	Ile	Thr	Ser	Pro	Phe	Tyr	Gly	Asp		
		370				375					380						
aaa	tct	act	gaa	cct	gta	caa	aag	cta	agc	ttt	gat	gga	caa	aaa	gtt	1200	
Lys	Ser	Thr	Glu	Pro	Val	Gln	Lys	Leu	Ser	Phe	Asp	Gly	Gln	Lys	Val		
385					390					395					400		
tat	cga	act	ata	gct	aat	aca	gac	gta	gcg	gct	tgg	ccg	aat	ggt	aag	1248	
Tyr	Arg	Thr	Ile	Ala	Asn	Thr	Asp	Val	Ala	Ala	Trp	Pro	Asn	Gly	Lys		
				405					410					415			
gta	tat	tta	ggt	gtt	acg	aaa	gtt	gat	ttt	agt	caa	tat	gat	gat	caa	1296	
Val	Tyr	Leu	Gly	Val	Thr	Lys	Val	Asp	Phe	Ser	Gln	Tyr	Asp	Asp	Gln		
			420					425					430				
aaa	aat	gaa	act	agt	aca	caa	aca	tat	gat	tca	aaa	aga	aac	aat	ggc	1344	
Lys	Asn	Glu	Thr	Ser	Thr	Gln	Thr	Tyr	Asp	Ser	Lys	Arg	Asn	Asn	Gly		



435	440	445	
cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr 450 455 460			1392
gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu 465 470 475 480			1440
tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp 485 490 495			1488
aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile 500 505 510			1536
act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser 515 520 525			1584
att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys 530 535 540			1632
gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala 545 550 555 560			1680
gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr 565 570 575			1728
aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile 580 585 590			1776
tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr 595 600 605			1824
ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys 610 615 620			1872
aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile 625 630 635 640			1920
tat ata gat aag ata gaa ttt atc cca gta caa ttg taa Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu 645 650			1959

<210> 20  
<211> 652

<212> PRT

<213> Artificial sequence

<220>

<223> Recombinant delta endotoxin

<400> 20

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro  
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Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn  
20 25 30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met  
35 40 45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp  
50 55 60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val  
65 70 75 80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu  
85 90 95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala  
100 105 110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser  
115 120 125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr  
130 135 140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser  
145 150 155 160

Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser  
165 170 175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val  
180 185 190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu  
195 200 205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu  
210 215 220

Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr  
225 230 235 240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg  
245 250 255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu

260					265					270					
Met	Thr	Leu	Thr	Val	Leu	Asp	Leu	Ile	Val	Leu	Phe	Pro	Phe	Tyr	Asp
		275					280					285			
Ile	Arg	Leu	Tyr	Ser	Lys	Gly	Val	Lys	Thr	Glu	Leu	Thr	Arg	Asp	Ile
		290				295					300				
Phe	Thr	Asp	Pro	Ile	Phe	Ala	Val	Asn	Thr	Leu	Trp	Glu	Tyr	Gly	Pro
305					310					315					320
Thr	Phe	Leu	Ser	Ile	Glu	Asn	Ser	Ile	Arg	Lys	Pro	His	Leu	Phe	Asp
				325					330					335	
Tyr	Leu	Gln	Gly	Ile	Glu	Phe	His	Thr	Arg	Leu	Gln	Pro	Gly	Tyr	Phe
			340					345					350		
Gly	Lys	Asp	Ser	Phe	Asn	Tyr	Trp	Ser	Gly	Asn	Tyr	Val	Glu	Thr	Arg
		355					360					365			
Pro	Ser	Ile	Gly	Ser	Ser	Lys	Thr	Ile	Thr	Ser	Pro	Phe	Tyr	Gly	Asp
		370				375					380				
Lys	Ser	Thr	Glu	Pro	Val	Gln	Lys	Leu	Ser	Phe	Asp	Gly	Gln	Lys	Val
385					390					395					400
Tyr	Arg	Thr	Ile	Ala	Asn	Thr	Asp	Val	Ala	Ala	Trp	Pro	Asn	Gly	Lys
				405					410					415	
Val	Tyr	Leu	Gly	Val	Thr	Lys	Val	Asp	Phe	Ser	Gln	Tyr	Asp	Asp	Gln
			420					425					430		
Lys	Asn	Glu	Thr	Ser	Thr	Gln	Thr	Tyr	Asp	Ser	Lys	Arg	Asn	Asn	Gly
		435					440					445			
His	Val	Ser	Ala	Gln	Asp	Ser	Ile	Asp	Gln	Leu	Pro	Pro	Glu	Thr	Thr
		450				455					460				
Asp	Glu	Pro	Leu	Glu	Lys	Ala	Tyr	Ser	His	Gln	Leu	Asn	Tyr	Ala	Glu
465					470					475					480
Cys	Phe	Leu	Met	Gln	Asp	Arg	Arg	Gly	Thr	Ile	Pro	Phe	Phe	Thr	Trp
				485					490					495	
Thr	His	Arg	Ser	Val	Asp	Phe	Phe	Asn	Thr	Ile	Asp	Ala	Glu	Lys	Ile
			500					505					510		
Thr	Gln	Leu	Pro	Val	Val	Lys	Ala	Tyr	Ala	Leu	Ser	Ser	Gly	Ala	Ser
		515					520					525			
Ile	Ile	Glu	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Asn	Leu	Leu	Phe	Leu	Lys
		530				535					540				
Glu	Ser	Ser	Asn	Ser	Ile	Ala	Lys	Phe	Lys	Val	Thr	Leu	Asn	Ser	Ala
545					550					555					560
Ala	Leu	Leu	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg	Tyr	Ala	Ser	Thr	Thr

	565		570		575
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile	580	585		590	
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr	595	600		605	
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys	610	615		620	
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile	625	630		635	640
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu	645	650			

<210> 21  
 <211> 1959  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Recombinant delta endotoxin

<220>  
 <221> CDS  
 <222> (1)..(1956)

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aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat	96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn	
20 25 30	
cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg	144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met	
35 40 45	
act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat	192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp	
50 55 60	
gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta	240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val	
65 70 75 80	
gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt	288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu	
85 90 95	
aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca	336

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala	
100 105 110	
caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt	384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser	
115 120 125	
aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat	432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr	
130 135 140	
ggt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt	480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser	
145 150 155 160	
aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt	528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser	
165 170 175	
cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg	576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val	
180 185 190	
ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta	624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu	
195 200 205	
tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa	672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu	
210 215 220	
gat gtt gct gaa ttc tat cgt aga caa tta aaa ctt aca caa caa tac	720
Asp Val Ala Glu Phe Tyr Arg Arg Gln Leu Lys Leu Thr Gln Gln Tyr	
225 230 235 240	
act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga	768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg	
245 250 255	
ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa	816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu	
260 265 270	
atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat	864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp	
275 280 285	
att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att	912
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile	
290 295 300	
ttt acg gat cca att ttt tta ctt act acg ctt cag aag tac gga cca	960
Phe Thr Asp Pro Ile Phe Leu Leu Thr Thr Leu Gln Lys Tyr Gly Pro	
305 310 315 320	
act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat	1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp	

325										330					335					
tat	tta	cag	ggg	att	gaa	ttt	cat	acg	cgt	ctt	caa	cct	ggt	tac	ttt	1056				
Tyr	Leu	Gln	Gly	Ile	Glu	Phe	His	Thr	Arg	Leu	Gln	Pro	Gly	Tyr	Phe					
			340						345				350							
ggg	aaa	gat	tct	ttc	aat	tat	tgg	tct	ggt	aat	tat	gta	gaa	act	aga	1104				
Gly	Lys	Asp	Ser	Phe	Asn	Tyr	Trp	Ser	Gly	Asn	Tyr	Val	Glu	Thr	Arg					
		355					360					365								
cct	agt	ata	gga	tct	agt	aag	aca	att	act	tcc	cca	ttt	tat	gga	gat	1152				
Pro	Ser	Ile	Gly	Ser	Ser	Lys	Thr	Ile	Thr	Ser	Pro	Phe	Tyr	Gly	Asp					
		370				375					380									
aaa	tct	act	gaa	cct	gta	caa	aag	cta	agc	ttt	gat	gga	caa	aaa	gtt	1200				
Lys	Ser	Thr	Glu	Pro	Val	Gln	Lys	Leu	Ser	Phe	Asp	Gly	Gln	Lys	Val					
					390					395					400					
tat	cga	act	ata	gct	aat	aca	gac	gta	gcg	gct	tgg	ccg	aat	ggt	aag	1248				
Tyr	Arg	Thr	Ile	Ala	Asn	Thr	Asp	Val	Ala	Ala	Trp	Pro	Asn	Gly	Lys					
				405					410					415						
gta	tat	tta	ggt	gtt	acg	aaa	gtt	gat	ttt	agt	caa	tat	gat	gat	caa	1296				
Val	Tyr	Leu	Gly	Val	Thr	Lys	Val	Asp	Phe	Ser	Gln	Tyr	Asp	Asp	Gln					
			420					425					430							
aaa	aat	gaa	act	agt	aca	caa	aca	tat	gat	tca	aaa	aga	aac	aat	ggc	1344				
Lys	Asn	Glu	Thr	Ser	Thr	Gln	Thr	Tyr	Asp	Ser	Lys	Arg	Asn	Asn	Gly					
		435					440					445								
cat	gta	agt	gca	cag	gat	tct	att	gac	caa	tta	ccg	cca	gaa	aca	aca	1392				
His	Val	Ser	Ala	Gln	Asp	Ser	Ile	Asp	Gln	Leu	Pro	Pro	Glu	Thr	Thr					
			450			455					460									
gat	gaa	cca	ctt	gaa	aaa	gca	tat	agt	cat	cag	ctt	aat	tac	gcg	gaa	1440				
Asp	Glu	Pro	Leu	Glu	Lys	Ala	Tyr	Ser	His	Gln	Leu	Asn	Tyr	Ala	Glu					
					470					475					480					
tgt	ttc	tta	atg	cag	gac	cgt	cgt	gga	aca	att	cca	ttt	ttt	act	tgg	1488				
Cys	Phe	Leu	Met	Gln	Asp	Arg	Arg	Gly	Thr	Ile	Pro	Phe	Phe	Thr	Trp					
				485					490					495						
aca	cat	aga	agt	gta	gac	ttt	ttt	aat	aca	att	gat	gct	gaa	aag	att	1536				
Thr	His	Arg	Ser	Val	Asp	Phe	Phe	Asn	Thr	Ile	Asp	Ala	Glu	Lys	Ile					
			500					505					510							
act	caa	ctt	cca	gta	gtg	aaa	gca	tat	gcc	ttg	tct	tca	ggt	gct	tcc	1584				
Thr	Gln	Leu	Pro	Val	Val	Lys	Ala	Tyr	Ala	Leu	Ser	Ser	Gly	Ala	Ser					
			515				520					525								
att	att	gaa	ggt	cca	gga	ttc	aca	gga	gga	aat	tta	cta	ttc	cta	aaa	1632				
Ile	Ile	Glu	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Asn	Leu	Leu	Phe	Leu	Lys					
		530				535					540									
gaa	tct	agt	aat	tca	att	gct	aaa	ttt	aaa	gtt	aca	tta	aat	tca	gca	1680				
Glu	Ser	Ser	Asn	Ser	Ile	Ala	Lys	Phe	Lys	Val	Thr	Leu	Asn	Ser	Ala					
					550					555					560					

gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act 1728  
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr  
565 570 575

aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc 1776  
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile  
580 585 590

tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca 1824  
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr  
595 600 605

ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag 1872  
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys  
610 615 620

aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc 1920  
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile  
625 630 635 640

tat ata gat aag ata gaa ttt atc cca gta caa ttg taa 1959  
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu  
645 650

<210> 22  
<211> 652  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Recombinant delta endotoxin

<400> 22

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro  
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Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn  
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Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met  
35 40 45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp  
50 55 60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val  
65 70 75 80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu  
85 90 95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala  
100 105 110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser  
 115 120 125  
 Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr  
 130 135 140  
 Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser  
 145 150 155 160  
 Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser  
 165 170 175  
 His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val  
 180 185 190  
 Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu  
 195 200 205  
 Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu  
 210 215 220  
 Asp Val Ala Glu Phe Tyr Arg Arg Gln Leu Lys Leu Thr Gln Gln Tyr  
 225 230 235 240  
 Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg  
 245 250 255  
 Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu  
 260 265 270  
 Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp  
 275 280 285  
 Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile  
 290 295 300  
 Phe Thr Asp Pro Ile Phe Leu Leu Thr Thr Leu Gln Lys Tyr Gly Pro  
 305 310 315 320  
 Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp  
 325 330 335  
 Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe  
 340 345 350  
 Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg  
 355 360 365  
 Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp  
 370 375 380  
 Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val  
 385 390 395 400  
 Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys  
 405 410 415



Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln  
 420 425 430  
 Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly  
 435 440 445  
 His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr  
 450 455 460  
 Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu  
 465 470 475 480  
 Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp  
 485 490 495  
 Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile  
 500 505 510  
 Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser  
 515 520 525  
 Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys  
 530 535 540  
 Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala  
 545 550 555 560  
 Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr  
 565 570 575  
 Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile  
 580 585 590  
 Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr  
 595 600 605  
 Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys  
 610 615 620  
 Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile  
 625 630 635 640  
 Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu  
 645 650

<210> 23  
 <211> 1959  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Recombinant delta endotoxin

<220>  
 <221> CDS

<222> (1)..(1956)

<400> 23

atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct	48
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro	
1 5 10 15	
aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat	96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn	
20 25 30	
cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg	144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met	
35 40 45	
act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat	192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp	
50 55 60	
gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta	240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val	
65 70 75 80	
gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt	288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu	
85 90 95	
aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca	336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala	
100 105 110	
caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt	384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser	
115 120 125	
aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat	432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr	
130 135 140	
gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt	480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser	
145 150 155 160	
aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt	528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser	
165 170 175	
cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg	576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val	
180 185 190	
ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta	624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu	
195 200 205	
tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa	672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu	

210	215	220	
gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac			720
Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr			
225	230	235	240
act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga			768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg			
	245	250	255
ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa			816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu			
	260	265	270
atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat			864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp			
	275	280	285
att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att			912
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile			
	290	295	300
ttt acg gat cca att ttt acg cca acc acc cta cag gat tac gga cca			960
Phe Thr Asp Pro Ile Phe Thr Pro Thr Thr Leu Gln Asp Tyr Gly Pro			
305	310	315	320
act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat			1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp			
	325	330	335
tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt			1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe			
	340	345	350
ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga			1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg			
	355	360	365
cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat			1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp			
	370	375	380
aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt			1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val			
385	390	395	400
tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag			1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys			
	405	410	415
gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa			1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln			
	420	425	430
aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc			1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly			
	435	440	445

cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr 450 455 460	1392
gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu 465 470 475 480	1440
tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp 485 490 495	1488
aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile 500 505 510	1536
act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser 515 520 525	1584
att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys 530 535 540	1632
gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala 545 550 555 560	1680
gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr 565 570 575	1728
aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile 580 585 590	1776
tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr 595 600 605	1824
ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys 610 615 620	1872
aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile 625 630 635 640	1920
tat ata gat aag ata gaa ttt atc cca gta caa ttg taa Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu 645 650	1959

<210> 24  
<211> 652  
<212> PRT

<213> Artificial sequence

<220>

<223> Recombinant delta endotoxin

<400> 24

Met	Asn	Pro	Asn	Asn	Arg	Ser	Glu	His	Asp	Thr	Ile	Lys	Val	Thr	Pro	
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Asn	Ser	Glu	Leu	Gln	Thr	Asn	His	Asn	Gln	Tyr	Pro	Leu	Ala	Asp	Asn	
			20					25					30			
Pro	Asn	Ser	Thr	Leu	Glu	Glu	Leu	Asn	Tyr	Lys	Glu	Phe	Leu	Arg	Met	
		35					40					45				
Thr	Glu	Asp	Ser	Ser	Thr	Glu	Val	Leu	Asp	Asn	Ser	Thr	Val	Lys	Asp	
	50					55					60					
Ala	Val	Gly	Thr	Gly	Ile	Ser	Val	Val	Gly	Gln	Ile	Leu	Gly	Val	Val	
65					70				75						80	
Gly	Val	Pro	Phe	Ala	Gly	Ala	Leu	Thr	Ser	Phe	Tyr	Gln	Ser	Phe	Leu	
				85					90					95		
Asn	Thr	Ile	Trp	Pro	Ser	Asp	Ala	Asp	Pro	Trp	Lys	Ala	Phe	Met	Ala	
			100					105					110			
Gln	Val	Glu	Val	Leu	Ile	Asp	Lys	Lys	Ile	Glu	Glu	Tyr	Ala	Lys	Ser	
		115					120					125				
Lys	Ala	Leu	Ala	Glu	Leu	Gln	Gly	Leu	Gln	Asn	Asn	Phe	Glu	Asp	Tyr	
	130					135					140					
Val	Asn	Ala	Leu	Asn	Ser	Trp	Lys	Lys	Thr	Pro	Leu	Ser	Leu	Arg	Ser	
145					150					155					160	
Lys	Arg	Ser	Gln	Asp	Arg	Ile	Arg	Glu	Leu	Phe	Ser	Gln	Ala	Glu	Ser	
				165					170					175		
His	Phe	Arg	Asn	Ser	Met	Pro	Ser	Phe	Ala	Val	Ser	Lys	Phe	Glu	Val	
			180					185					190			
Leu	Phe	Leu	Pro	Thr	Tyr	Ala	Gln	Ala	Ala	Asn	Thr	His	Leu	Leu	Leu	
		195					200					205				
Leu	Lys	Asp	Ala	Gln	Val	Phe	Gly	Glu	Glu	Trp	Gly	Tyr	Ser	Ser	Glu	
	210					215					220					
Asp	Val	Ala	Glu	Phe	Tyr	His	Arg	Gln	Leu	Lys	Leu	Thr	Gln	Gln	Tyr	
225					230					235					240	
Thr	Asp	His	Cys	Val	Asn	Trp	Tyr	Asn	Val	Gly	Leu	Asn	Gly	Leu	Arg	
				245					250					255		
Gly	Ser	Thr	Tyr	Asp	Ala	Trp	Val	Lys	Phe	Asn	Arg	Phe	Arg	Arg	Glu	
			260					265					270			

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp  
 275 280 285  
 Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile  
 290 300  
 Phe Thr Asp Pro Ile Phe Thr Pro Thr Thr Leu Gln Asp Tyr Gly Pro  
 305 310 315 320  
 Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp  
 325 330 335  
 Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe  
 340 345 350  
 Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg  
 355 360 365  
 Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp  
 370 375 380  
 Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val  
 385 390 395 400  
 Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys  
 405 410 415  
 Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln  
 420 425 430  
 Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly  
 435 440 445  
 His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr  
 450 455 460  
 Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu  
 465 470 475 480  
 Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp  
 485 490 495  
 Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile  
 500 505 510  
 Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser  
 515 520 525  
 Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys  
 530 535 540  
 Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala  
 545 550 555 560  
 Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr  
 565 570 575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile  
 580 585 590  
 Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr  
 595 600 605  
 Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys  
 610 615 620  
 Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile  
 625 630 635 640  
 Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu  
 645 650

<210> 25  
 <211> 1959  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Recombinant delta endotoxin

<220>  
 <221> CDS  
 <222> (1)..(1956)

<400> 25  
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 aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat 96  
 Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn  
 20 25 30  
 cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg 144  
 Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met  
 35 40 45  
 act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat 192  
 Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp  
 50 55 60  
 gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta 240  
 Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val  
 65 70 75 80  
 gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt 288  
 Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu  
 85 90 95  
 aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca 336  
 Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala

100	105	110	
caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser 115 120 125			384
aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr 130 135 140			432
gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser 145 150 155 160			480
aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser 165 170 175			528
cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val 180 185 190			576
ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu 195 200 205			624
tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu 210 215 220			672
gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr 225 230 235 240			720
act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg 245 250 255			768
ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu 260 265 270			816
atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp 275 280 285			864
att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile 290 295 300			912
ttt acg gat cca att ttt gcc ctg aat acc tta gac gag tac gga cca Phe Thr Asp Pro Ile Phe Ala Leu Asn Thr Leu Asp Glu Tyr Gly Pro 305 310 315 320			960
act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp 325 330 335			1008



tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe 340 345 350	1056
ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg 355 360 365	1104
cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp 370 375 380	1152
aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val 385 390 395 400	1200
tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys 405 410 415	1248
gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln 420 425 430	1296
aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly 435 440 445	1344
cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr 450 455 460	1392
gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu 465 470 475 480	1440
tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp 485 490 495	1488
aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile 500 505 510	1536
act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser 515 520 525	1584
att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys 530 535 540	1632
gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala 545 550 555 560	1680

gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act 1728  
 Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr  
 565 570 575

aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc 1776  
 Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile  
 580 585 590

tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca 1824  
 Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr  
 595 600 605

ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag 1872  
 Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys  
 610 615 620

aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc 1920  
 Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile  
 625 630 635 640

tat ata gat aag ata gaa ttt atc cca gta caa ttg taa 1959  
 Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu  
 645 650

<210> 26  
 <211> 652  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Recombinant delta endotoxin

<400> 26

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro  
 1 5 10 15

Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn  
 20 25 30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met  
 35 40 45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp  
 50 55 60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val  
 65 70 75 80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu  
 85 90 95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala  
 100 105 110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser

115					120					125					
Lys	Ala	Leu	Ala	Glu	Leu	Gln	Gly	Leu	Gln	Asn	Asn	Phe	Glu	Asp	Tyr
130					135					140					
Val	Asn	Ala	Leu	Asn	Ser	Trp	Lys	Lys	Thr	Pro	Leu	Ser	Leu	Arg	Ser
145					150					155					
Lys	Arg	Ser	Gln	Asp	Arg	Ile	Arg	Glu	Leu	Phe	Ser	Gln	Ala	Glu	Ser
165					170					175					
His	Phe	Arg	Asn	Ser	Met	Pro	Ser	Phe	Ala	Val	Ser	Lys	Phe	Glu	Val
180					185					190					
Leu	Phe	Leu	Pro	Thr	Tyr	Ala	Gln	Ala	Ala	Asn	Thr	His	Leu	Leu	Leu
195					200					205					
Leu	Lys	Asp	Ala	Gln	Val	Phe	Gly	Glu	Glu	Trp	Gly	Tyr	Ser	Ser	Glu
210					215					220					
Asp	Val	Ala	Glu	Phe	Tyr	His	Arg	Gln	Leu	Lys	Leu	Thr	Gln	Gln	Tyr
225					230					235					
Thr	Asp	His	Cys	Val	Asn	Trp	Tyr	Asn	Val	Gly	Leu	Asn	Gly	Leu	Arg
245					250					255					
Gly	Ser	Thr	Tyr	Asp	Ala	Trp	Val	Lys	Phe	Asn	Arg	Phe	Arg	Arg	Glu
260					265					270					
Met	Thr	Leu	Thr	Val	Leu	Asp	Leu	Ile	Val	Leu	Phe	Pro	Phe	Tyr	Asp
275					280					285					
Ile	Arg	Leu	Tyr	Ser	Lys	Gly	Val	Lys	Thr	Glu	Leu	Thr	Arg	Asp	Ile
290					295					300					
Phe	Thr	Asp	Pro	Ile	Phe	Ala	Leu	Asn	Thr	Leu	Asp	Glu	Tyr	Gly	Pro
305					310					315					
Thr	Phe	Leu	Ser	Ile	Glu	Asn	Ser	Ile	Arg	Lys	Pro	His	Leu	Phe	Asp
325					330					335					
Tyr	Leu	Gln	Gly	Ile	Glu	Phe	His	Thr	Arg	Leu	Gln	Pro	Gly	Tyr	Phe
340					345					350					
Gly	Lys	Asp	Ser	Phe	Asn	Tyr	Trp	Ser	Gly	Asn	Tyr	Val	Glu	Thr	Arg
355					360					365					
Pro	Ser	Ile	Gly	Ser	Ser	Lys	Thr	Ile	Thr	Ser	Pro	Phe	Tyr	Gly	Asp
370					375					380					
Lys	Ser	Thr	Glu	Pro	Val	Gln	Lys	Leu	Ser	Phe	Asp	Gly	Gln	Lys	Val
385					390					395					
Tyr	Arg	Thr	Ile	Ala	Asn	Thr	Asp	Val	Ala	Ala	Trp	Pro	Asn	Gly	Lys
405					410					415					
Val	Tyr	Leu	Gly	Val	Thr	Lys	Val	Asp	Phe	Ser	Gln	Tyr	Asp	Asp	Gln

420					425					430					
Lys	Asn	Glu	Thr	Ser	Thr	Gln	Thr	Tyr	Asp	Ser	Lys	Arg	Asn	Asn	Gly
	435					440					445				
His	Val	Ser	Ala	Gln	Asp	Ser	Ile	Asp	Gln	Leu	Pro	Pro	Glu	Thr	Thr
	450					455					460				
Asp	Glu	Pro	Leu	Glu	Lys	Ala	Tyr	Ser	His	Gln	Leu	Asn	Tyr	Ala	Glu
465					470					475					480
Cys	Phe	Leu	Met	Gln	Asp	Arg	Arg	Gly	Thr	Ile	Pro	Phe	Phe	Thr	Trp
				485					490					495	
Thr	His	Arg	Ser	Val	Asp	Phe	Phe	Asn	Thr	Ile	Asp	Ala	Glu	Lys	Ile
			500					505					510		
Thr	Gln	Leu	Pro	Val	Val	Lys	Ala	Tyr	Ala	Leu	Ser	Ser	Gly	Ala	Ser
		515					520					525			
Ile	Ile	Glu	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Asn	Leu	Leu	Phe	Leu	Lys
	530					535					540				
Glu	Ser	Ser	Asn	Ser	Ile	Ala	Lys	Phe	Lys	Val	Thr	Leu	Asn	Ser	Ala
545					550					555					560
Ala	Leu	Leu	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg	Tyr	Ala	Ser	Thr	Thr
				565					570					575	
Asn	Leu	Arg	Leu	Phe	Val	Gln	Asn	Ser	Asn	Asn	Asp	Phe	Leu	Val	Ile
			580					585					590		
Tyr	Ile	Asn	Lys	Thr	Met	Asn	Lys	Asp	Asp	Asp	Leu	Thr	Tyr	Gln	Thr
		595					600					605			
Phe	Asp	Leu	Ala	Thr	Thr	Asn	Ser	Asn	Met	Gly	Phe	Ser	Gly	Asp	Lys
	610					615					620				
Asn	Glu	Leu	Ile	Ile	Gly	Ala	Glu	Ser	Phe	Val	Ser	Asn	Glu	Lys	Ile
625					630					635					640
Tyr	Ile	Asp	Lys	Ile	Glu	Phe	Ile	Pro	Val	Gln	Leu				
			645						650						

<210> 27

<211> 1959

<212> DNA

<213> Artificial sequence

<220>

<223> Recombinant delta endotoxin

<220>

<221> CDS

<222> (1)..(1956)

<400> 27

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Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro	
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aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat	96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn	
20 25 30	
cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg	144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met	
35 40 45	
act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat	192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp	
50 55 60	
gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta	240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val	
65 70 75 80	
gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt	288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu	
85 90 95	
aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca	336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala	
100 105 110	
caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt	384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser	
115 120 125	
aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat	432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr	
130 135 140	
gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt	480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser	
145 150 155 160	
aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt	528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser	
165 170 175	
cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg	576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val	
180 185 190	
ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta	624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu	
195 200 205	
tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa	672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu	
210 215 220	

gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr 225 230 235 240	720
act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg 245 250 255	768
ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu 260 265 270	816
atg act tta act gta tta gat cta att gta ctt ttc cca ttt tac gat Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp 275 280 285	864
act agg cga ttc aga aag ggg gtt aaa aca gaa cta aca aga gac att Thr Arg Arg Phe Arg Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile 290 295 300	912
ttt acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro 305 310 315 320	960
act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp 325 330 335	1008
tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe 340 345 350	1056
ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg 355 360 365	1104
cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp 370 375 380	1152
aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val 385 390 395 400	1200
tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys 405 410 415	1248
gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln 420 425 430	1296
aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly 435 440 445	1344

cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca	1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr	
450 455 460	
gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa	1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu	
465 470 475 480	
tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg	1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp	
485 490 495	
aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att	1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile	
500 505 510	
act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc	1584
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser	
515 520 525	
att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa	1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys	
530 535 540	
gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca	1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala	
545 550 555 560	
gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act	1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr	
565 570 575	
aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc	1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile	
580 585 590	
tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca	1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr	
595 600 605	
ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag	1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys	
610 615 620	
aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc	1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile	
625 630 635 640	
tat ata gat aag ata gaa ttt atc cca gta caa ttg taa	1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu	
645 650	

<210> 28  
 <211> 652  
 <212> PRT  
 <213> Artificial sequence

<220>

<223> Recombinant delta endotoxin

<400> 28

Met	Asn	Pro	Asn	Asn	Arg	Ser	Glu	His	Asp	Thr	Ile	Lys	Val	Thr	Pro	
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Asn	Ser	Glu	Leu	Gln	Thr	Asn	His	Asn	Gln	Tyr	Pro	Leu	Ala	Asp	Asn	
			20					25					30			
Pro	Asn	Ser	Thr	Leu	Glu	Glu	Leu	Asn	Tyr	Lys	Glu	Phe	Leu	Arg	Met	
		35					40					45				
Thr	Glu	Asp	Ser	Ser	Thr	Glu	Val	Leu	Asp	Asn	Ser	Thr	Val	Lys	Asp	
	50					55					60					
Ala	Val	Gly	Thr	Gly	Ile	Ser	Val	Val	Gly	Gln	Ile	Leu	Gly	Val	Val	
65					70					75					80	
Gly	Val	Pro	Phe	Ala	Gly	Ala	Leu	Thr	Ser	Phe	Tyr	Gln	Ser	Phe	Leu	
				85					90					95		
Asn	Thr	Ile	Trp	Pro	Ser	Asp	Ala	Asp	Pro	Trp	Lys	Ala	Phe	Met	Ala	
			100					105					110			
Gln	Val	Glu	Val	Leu	Ile	Asp	Lys	Lys	Ile	Glu	Glu	Tyr	Ala	Lys	Ser	
		115					120					125				
Lys	Ala	Leu	Ala	Glu	Leu	Gln	Gly	Leu	Gln	Asn	Asn	Phe	Glu	Asp	Tyr	
	130					135					140					
Val	Asn	Ala	Leu	Asn	Ser	Trp	Lys	Lys	Thr	Pro	Leu	Ser	Leu	Arg	Ser	
145					150					155					160	
Lys	Arg	Ser	Gln	Asp	Arg	Ile	Arg	Glu	Leu	Phe	Ser	Gln	Ala	Glu	Ser	
				165					170					175		
His	Phe	Arg	Asn	Ser	Met	Pro	Ser	Phe	Ala	Val	Ser	Lys	Phe	Glu	Val	
			180					185					190			
Leu	Phe	Leu	Pro	Thr	Tyr	Ala	Gln	Ala	Ala	Asn	Thr	His	Leu	Leu	Leu	
		195					200					205				
Leu	Lys	Asp	Ala	Gln	Val	Phe	Gly	Glu	Glu	Trp	Gly	Tyr	Ser	Ser	Glu	
	210					215					220					
Asp	Val	Ala	Glu	Phe	Tyr	His	Arg	Gln	Leu	Lys	Leu	Thr	Gln	Gln	Tyr	
225					230					235					240	
Thr	Asp	His	Cys	Val	Asn	Trp	Tyr	Asn	Val	Gly	Leu	Asn	Gly	Leu	Arg	
				245					250					255		
Gly	Ser	Thr	Tyr	Asp	Ala	Trp	Val	Lys	Phe	Asn	Arg	Phe	Arg	Arg	Glu	
			260					265					270			



Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp  
 275 280 285

Thr Arg Arg Phe Arg Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile  
 290 295 300

Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro  
 305 310 315 320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp  
 325 330 335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe  
 340 345 350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg  
 355 360 365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp  
 370 375 380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val  
 385 390 395 400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys  
 405 410 415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln  
 420 425 430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly  
 435 440 445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr  
 450 455 460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu  
 465 470 475 480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp  
 485 490 495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile  
 500 505 510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser  
 515 520 525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys  
 530 535 540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala  
 545 550 555 560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr  
 565 570 575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile  
 580 585 590  
 Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr  
 595 600 605  
 Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys  
 610 615 620  
 Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile  
 625 630 635 640  
 Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu  
 645 650

<210> 29  
 <211> 1959  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> Recombinant delta endotoxin

<220>  
 <221> CDS  
 <222> (1)..(1956)

<400> 29  
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 aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat 96  
 Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn  
 20 25 30  
  
 cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg 144  
 Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met  
 35 40 45  
  
 act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat 192  
 Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp  
 50 55 60  
  
 gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta 240  
 Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val  
 65 70 75 80  
  
 gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt 288  
 Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu  
 85 90 95  
  
 aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca 336  
 Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala  
 100 105 110

caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser 115 120 125	384
aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr 130 135 140	432
gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser 145 150 155 160	480
aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser 165 170 175	528
cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val 180 185 190	576
ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu 195 200 205	624
tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu 210 215 220	672
gat gtt gct gaa ttc tat cgt aga caa tta aaa ctt aca caa caa tac Asp Val Ala Glu Phe Tyr Arg Arg Gln Leu Lys Leu Thr Gln Gln Tyr 225 230 235 240	720
act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg 245 250 255	768
ggg tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu 260 265 270	816
atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp 275 280 285	864
att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile 290 295 300	912
ttt acg gat cca att ttt tta ctt aat act ctt cag gag tat gga cca Phe Thr Asp Pro Ile Phe Leu Leu Asn Thr Leu Gln Glu Tyr Gly Pro 305 310 315 320	960
act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp 325 330 335	1008

tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe 340 345 350	1056
ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg 355 360 365	1104
cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp 370 375 380	1152
aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val 385 390 395 400	1200
tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys 405 410 415	1248
gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln 420 425 430	1296
aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly 435 440 445	1344
cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr 450 455 460	1392
gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu 465 470 475 480	1440
tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp 485 490 495	1488
aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile 500 505 510	1536
act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser 515 520 525	1584
att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys 530 535 540	1632
gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala 545 550 555 560	1680
gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act	1728

Ala	Leu	Leu	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg	Tyr	Ala	Ser	Thr	Thr		
				565					570					575			
aac	tta	cga	ctt	ttt	gtg	caa	aat	tca	aac	aat	gat	ttt	ctt	gtc	atc	1776	
Asn	Leu	Arg	Leu	Phe	Val	Gln	Asn	Ser	Asn	Asn	Asp	Phe	Leu	Val	Ile		
			580					585					590				
tac	att	aat	aaa	act	atg	aat	aaa	gat	gat	gat	tta	aca	tat	caa	aca	1824	
Tyr	Ile	Asn	Lys	Thr	Met	Asn	Lys	Asp	Asp	Asp	Leu	Thr	Tyr	Gln	Thr		
			595					600					605				
ttt	gat	ctc	gca	act	act	aat	tct	aat	atg	ggg	ttc	tcg	ggt	gat	aag	1872	
Phe	Asp	Leu	Ala	Thr	Thr	Asn	Ser	Asn	Met	Gly	Phe	Ser	Gly	Asp	Lys		
	610						615				620						
aat	gaa	ctt	ata	ata	gga	gca	gaa	tct	ttc	gtt	tct	aat	gaa	aaa	atc	1920	
Asn	Glu	Leu	Ile	Ile	Gly	Ala	Glu	Ser	Phe	Val	Ser	Asn	Glu	Lys	Ile		
	625					630				635					640		
tat	ata	gat	aag	ata	gaa	ttt	atc	cca	gta	caa	ttg	taa				1959	
Tyr	Ile	Asp	Lys	Ile	Glu	Phe	Ile	Pro	Val	Gln	Leu						
				645					650								

<210> 30  
 <211> 652  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Recombinant delta endotoxin

<400> 30

Met	Asn	Pro	Asn	Asn	Arg	Ser	Glu	His	Asp	Thr	Ile	Lys	Val	Thr	Pro		
1				5					10					15			
Asn	Ser	Glu	Leu	Gln	Thr	Asn	His	Asn	Gln	Tyr	Pro	Leu	Ala	Asp	Asn		
			20					25					30				
Pro	Asn	Ser	Thr	Leu	Glu	Glu	Leu	Asn	Tyr	Lys	Glu	Phe	Leu	Arg	Met		
		35					40					45					
Thr	Glu	Asp	Ser	Ser	Thr	Glu	Val	Leu	Asp	Asn	Ser	Thr	Val	Lys	Asp		
	50					55					60						
Ala	Val	Gly	Thr	Gly	Ile	Ser	Val	Val	Gly	Gln	Ile	Leu	Gly	Val	Val		
	65				70					75					80		
Gly	Val	Pro	Phe	Ala	Gly	Ala	Leu	Thr	Ser	Phe	Tyr	Gln	Ser	Phe	Leu		
				85					90					95			
Asn	Thr	Ile	Trp	Pro	Ser	Asp	Ala	Asp	Pro	Trp	Lys	Ala	Phe	Met	Ala		
			100					105						110			
Gln	Val	Glu	Val	Leu	Ile	Asp	Lys	Lys	Ile	Glu	Glu	Tyr	Ala	Lys	Ser		
		115					120					125					

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr  
 130 135 140  
 Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser  
 145 150 155 160  
 Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser  
 165 170 175  
 His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val  
 180 185 190  
 Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu  
 195 200 205  
 Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu  
 210 215 220  
 Asp Val Ala Glu Phe Tyr Arg Arg Gln Leu Lys Leu Thr Gln Gln Tyr  
 225 230 235 240  
 Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg  
 245 250 255  
 Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu  
 260 265 270  
 Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp  
 275 280 285  
 Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile  
 290 295 300  
 Phe Thr Asp Pro Ile Phe Leu Leu Asn Thr Leu Gln Glu Tyr Gly Pro  
 305 310 315 320  
 Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp  
 325 330 335  
 Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe  
 340 345 350  
 Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg  
 355 360 365  
 Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp  
 370 375 380  
 Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val  
 385 390 395 400  
 Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys  
 405 410 415  
 Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln  
 420 425 430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly  
 435 440 445  
 His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr  
 450 455 460  
 Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu  
 465 470 475 480  
 Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp  
 485 490 495  
 Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile  
 500 505 510  
 Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser  
 515 520 525  
 Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys  
 530 535 540  
 Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala  
 545 550 555 560  
 Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr  
 565 570 575  
 Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile  
 580 585 590  
 Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr  
 595 600 605  
 Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys  
 610 615 620  
 Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile  
 625 630 635 640  
 Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu  
 645 650

<210> 31

<211> 1959

<212> DNA

<213> Artificial sequence

<220>

<223> Recombinant delta endotoxin

<220>

<221> CDS

<222> (1)..(1956)

<400> 31

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aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat	96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn	
20 25 30	
cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg	144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met	
35 40 45	
act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat	192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp	
50 55 60	
gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta	240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val	
65 70 75 80	
gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt	288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu	
85 90 95	
aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca	336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala	
100 105 110	
caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt	384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser	
115 120 125	
aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat	432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr	
130 135 140	
gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt	480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser	
145 150 155 160	
aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt	528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser	
165 170 175	
cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg	576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val	
180 185 190	
ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta	624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu	
195 200 205	
tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa	672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu	
210 215 220	



gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac	720
Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr	
225 230 235 240	
act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga	768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg	
245 250 255	
ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa	816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu	
260 265 270	
atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat	864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp	
275 280 285	
att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att	912
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile	
290 295 300	
ttt acg gat cca att ttt atc ctc aat acg cta cag gag tac gga cca	960
Phe Thr Asp Pro Ile Phe Ile Leu Asn Thr Leu Gln Glu Tyr Gly Pro	
305 310 315 320	
act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat	1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp	
325 330 335	
tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt	1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe	
340 345 350	
ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga	1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg	
355 360 365	
cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat	1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp	
370 375 380	
aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt	1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val	
385 390 395 400	
tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag	1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys	
405 410 415	
gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa	1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln	
420 425 430	
aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc	1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly	
435 440 445	
cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca	1392

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr	
450 455 460	
gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa	1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu	
465 470 475 480	
tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg	1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp	
485 490 495	
aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att	1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile	
500 505 510	
act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc	1584
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser	
515 520 525	
att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa	1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys	
530 535 540	
gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca	1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala	
545 550 555 560	
gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act	1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr	
565 570 575	
aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc	1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile	
580 585 590	
tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca	1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr	
595 600 605	
ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag	1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys	
610 615 620	
aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc	1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile	
625 630 635 640	
tat ata gat aag ata gaa ttt atc cca gta caa ttg taa	1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu	
645 650	

<210> 32  
 <211> 652  
 <212> PRT  
 <213> Artificial sequence

<220>

<223> Recombinant delta endotoxin

<400> 32

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro  
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Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn  
20 25 30  
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met  
35 40 45  
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp  
50 55 60  
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val  
65 70 75 80  
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu  
85 90 95  
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala  
100 105 110  
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser  
115 120 125  
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr  
130 135 140  
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser  
145 150 155 160  
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser  
165 170 175  
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val  
180 185 190  
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu  
195 200 205  
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu  
210 215 220  
Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr  
225 230 235 240  
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg  
245 250 255  
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu  
260 265 270  
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp

275					280					285					
Ile	Arg	Leu	Tyr	Ser	Lys	Gly	Val	Lys	Thr	Glu	Leu	Thr	Arg	Asp	Ile
290						295					300				
Phe	Thr	Asp	Pro	Ile	Phe	Ile	Leu	Asn	Thr	Leu	Gln	Glu	Tyr	Gly	Pro
305					310					315					320
Thr	Phe	Leu	Ser	Ile	Glu	Asn	Ser	Ile	Arg	Lys	Pro	His	Leu	Phe	Asp
				325					330					335	
Tyr	Leu	Gln	Gly	Ile	Glu	Phe	His	Thr	Arg	Leu	Gln	Pro	Gly	Tyr	Phe
			340					345					350		
Gly	Lys	Asp	Ser	Phe	Asn	Tyr	Trp	Ser	Gly	Asn	Tyr	Val	Glu	Thr	Arg
		355					360					365			
Pro	Ser	Ile	Gly	Ser	Ser	Lys	Thr	Ile	Thr	Ser	Pro	Phe	Tyr	Gly	Asp
		370				375					380				
Lys	Ser	Thr	Glu	Pro	Val	Gln	Lys	Leu	Ser	Phe	Asp	Gly	Gln	Lys	Val
385					390					395					400
Tyr	Arg	Thr	Ile	Ala	Asn	Thr	Asp	Val	Ala	Ala	Trp	Pro	Asn	Gly	Lys
				405				410						415	
Val	Tyr	Leu	Gly	Val	Thr	Lys	Val	Asp	Phe	Ser	Gln	Tyr	Asp	Asp	Gln
			420					425					430		
Lys	Asn	Glu	Thr	Ser	Thr	Gln	Thr	Tyr	Asp	Ser	Lys	Arg	Asn	Asn	Gly
		435					440					445			
His	Val	Ser	Ala	Gln	Asp	Ser	Ile	Asp	Gln	Leu	Pro	Pro	Glu	Thr	Thr
		450				455					460				
Asp	Glu	Pro	Leu	Glu	Lys	Ala	Tyr	Ser	His	Gln	Leu	Asn	Tyr	Ala	Glu
465					470					475					480
Cys	Phe	Leu	Met	Gln	Asp	Arg	Arg	Gly	Thr	Ile	Pro	Phe	Phe	Thr	Trp
				485				490						495	
Thr	His	Arg	Ser	Val	Asp	Phe	Phe	Asn	Thr	Ile	Asp	Ala	Glu	Lys	Ile
			500					505					510		
Thr	Gln	Leu	Pro	Val	Val	Lys	Ala	Tyr	Ala	Leu	Ser	Ser	Gly	Ala	Ser
			515				520					525			
Ile	Ile	Glu	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Asn	Leu	Leu	Phe	Leu	Lys
			530			535					540				
Glu	Ser	Ser	Asn	Ser	Ile	Ala	Lys	Phe	Lys	Val	Thr	Leu	Asn	Ser	Ala
545					550					555					560
Ala	Leu	Leu	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg	Tyr	Ala	Ser	Thr	Thr
				565				570						575	
Asn	Leu	Arg	Leu	Phe	Val	Gln	Asn	Ser	Asn	Asn	Asp	Phe	Leu	Val	Ile

580	585	590
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr		
595	600	605
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys		
610	615	620
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile		
625	630	635
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu		
645	650	

<210> 33  
 <211> 1959  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Recombinant delta endotoxin

<220>  
 <221> CDS  
 <222> (1)..(1956)

<400> 33	
atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct	48
Met Asn Pro Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro	
1 5 10 15	
aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat	96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn	
20 25 30	
cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg	144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met	
35 40 45	
act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat	192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp	
50 55 60	
gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta	240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val	
65 70 75 80	
gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt	288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu	
85 90 95	
aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca	336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala	
100 105 110	

caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser 115 120 125	384
aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr 130 135 140	432
gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser 145 150 155 160	480
aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser 165 170 175	528
cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val 180 185 190	576
ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu 195 200 205	624
tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu 210 215 220	672
gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr 225 230 235 240	720
act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg 245 250 255	768
ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu 260 265 270	816
atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp 275 280 285	864
att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile 290 295 300	912
ttt acg gat cca att ttt atc cta cat acg ctg cag gag tac gga cca Phe Thr Asp Pro Ile Phe Ile Leu His Thr Leu Gln Glu Tyr Gly Pro 305 310 315 320	960
act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp 325 330 335	1008
tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt	1056

Tyr	Leu	Gln	Gly	Ile	Glu	Phe	His	Thr	Arg	Leu	Gln	Pro	Gly	Tyr	Phe		
			340					345					350				
ggg	aaa	gat	tct	ttc	aat	tat	tgg	tct	ggt	aat	tat	gta	gaa	act	aga	1104	
Gly	Lys	Asp	Ser	Phe	Asn	Tyr	Trp	Ser	Gly	Asn	Tyr	Val	Glu	Thr	Arg		
		355					360					365					
cct	agt	ata	gga	tct	agt	aag	aca	att	act	tcc	cca	ttt	tat	gga	gat	1152	
Pro	Ser	Ile	Gly	Ser	Ser	Lys	Thr	Ile	Thr	Ser	Pro	Phe	Tyr	Gly	Asp		
	370					375					380						
aaa	tct	act	gaa	cct	gta	caa	aag	cta	agc	ttt	gat	gga	caa	aaa	gtt	1200	
Lys	Ser	Thr	Glu	Pro	Val	Gln	Lys	Leu	Ser	Phe	Asp	Gly	Gln	Lys	Val		
385					390					395					400		
tat	cga	act	ata	gct	aat	aca	gac	gta	gcg	gct	tgg	ccg	aat	ggt	aag	1248	
Tyr	Arg	Thr	Ile	Ala	Asn	Thr	Asp	Val	Ala	Ala	Trp	Pro	Asn	Gly	Lys		
				405					410					415			
gta	tat	tta	ggg	gtt	acg	aaa	gtt	gat	ttt	agt	caa	tat	gat	gat	caa	1296	
Val	Tyr	Leu	Gly	Val	Thr	Lys	Val	Asp	Phe	Ser	Gln	Tyr	Asp	Asp	Gln		
			420					425					430				
aaa	aat	gaa	act	agt	aca	caa	aca	tat	gat	tca	aaa	aga	aac	aat	ggc	1344	
Lys	Asn	Glu	Thr	Ser	Thr	Gln	Thr	Tyr	Asp	Ser	Lys	Arg	Asn	Asn	Gly		
		435					440					445					
cat	gta	agt	gca	cag	gat	tct	att	gac	caa	tta	ccg	cca	gaa	aca	aca	1392	
His	Val	Ser	Ala	Gln	Asp	Ser	Ile	Asp	Gln	Leu	Pro	Pro	Glu	Thr	Thr		
	450					455					460						
gat	gaa	cca	ctt	gaa	aaa	gca	tat	agt	cat	cag	ctt	aat	tac	gcg	gaa	1440	
Asp	Glu	Pro	Leu	Glu	Lys	Ala	Tyr	Ser	His	Gln	Leu	Asn	Tyr	Ala	Glu		
465					470					475					480		
tgt	ttc	tta	atg	cag	gac	cgt	cgt	gga	aca	att	cca	ttt	ttt	act	tgg	1488	
Cys	Phe	Leu	Met	Gln	Asp	Arg	Arg	Gly	Thr	Ile	Pro	Phe	Phe	Thr	Trp		
				485				490						495			
aca	cat	aga	agt	gta	gac	ttt	ttt	aat	aca	att	gat	gct	gaa	aag	att	1536	
Thr	His	Arg	Ser	Val	Asp	Phe	Phe	Asn	Thr	Ile	Asp	Ala	Glu	Lys	Ile		
			500					505					510				
act	caa	ctt	cca	gta	gtg	aaa	gca	tat	gcc	ttg	tct	tca	ggg	gct	tcc	1584	
Thr	Gln	Leu	Pro	Val	Val	Lys	Ala	Tyr	Ala	Leu	Ser	Ser	Gly	Ala	Ser		
		515					520					525					
att	att	gaa	ggg	cca	gga	ttc	aca	gga	gga	aat	tta	cta	ttc	cta	aaa	1632	
Ile	Ile	Glu	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Asn	Leu	Leu	Phe	Leu	Lys		
	530					535					540						
gaa	tct	agt	aat	tca	att	gct	aaa	ttt	aaa	gtt	aca	tta	aat	tca	gca	1680	
Glu	Ser	Ser	Asn	Ser	Ile	Ala	Lys	Phe	Lys	Val	Thr	Leu	Asn	Ser	Ala		
545					550					555					560		
gcc	ttg	tta	caa	cga	tat	cgt	gta	aga	ata	cgc	tat	gct	tct	acc	act	1728	
Ala	Leu	Leu	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg	Tyr	Ala	Ser	Thr	Thr		

565	570	575	
aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile 580 585 590			1776
tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr 595 600 605			1824
ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys 610 615 620			1872
aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile 625 630 635 640			1920
tat ata gat aag ata gaa ttt atc cca gta caa ttg taa Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu 645 650			1959

<210> 34

<211> 652

<212> PRT

<213> Artificial sequence

<220>

<223> Recombinant delta endotoxin

<400> 34

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro 1 5 10 15
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn 20 25 30
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met 35 40 45
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp 50 55 60
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val 65 70 75 80
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu 85 90 95
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala 100 105 110
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser 115 120 125



Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr  
 130 135 140  
 Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser  
 145 150 155 160  
 Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser  
 165 170 175  
 His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val  
 180 185 190  
 Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu  
 195 200 205  
 Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu  
 210 215 220  
 Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr  
 225 230 235 240  
 Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg  
 245 250 255  
 Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu  
 260 265 270  
 Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp  
 275 280 285  
 Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile  
 290 295 300  
 Phe Thr Asp Pro Ile Phe Ile Leu His Thr Leu Gln Glu Tyr Gly Pro  
 305 310 315 320  
 Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp  
 325 330 335  
 Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe  
 340 345 350  
 Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg  
 355 360 365  
 Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp  
 370 375 380  
 Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val  
 385 390 395 400  
 Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys  
 405 410 415  
 Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln  
 420 425 430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly  
 435 440 445  
 His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr  
 450 455 460  
 Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu  
 465 470 475 480  
 Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp  
 485 490 495  
 Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile  
 500 505 510  
 Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser  
 515 520 525  
 Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys  
 530 535 540  
 Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala  
 545 550 555 560  
 Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr  
 565 570 575  
 Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile  
 580 585 590  
 Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr  
 595 600 605  
 Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys  
 610 615 620  
 Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile  
 625 630 635 640  
 Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu  
 645 650

<210> 35  
 <211> 1959  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Recombinant delta endotoxin

<220>  
 <221> CDS  
 <222> (1)..(1956)

<400> 35

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aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn 20 25 30	96
cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met 35 40 45	144
act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp 50 55 60	192
gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val 65 70 75 80	240
gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu 85 90 95	288
aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala 100 105 110	336
caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser 115 120 125	384
aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr 130 135 140	432
gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser 145 150 155 160	480
aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser 165 170 175	528
cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val 180 185 190	576
ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu 195 200 205	624
tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu 210 215 220	672
gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac	720

Asp	Val	Ala	Glu	Phe	Tyr	His	Arg	Gln	Leu	Lys	Leu	Thr	Gln	Gln	Tyr	
225					230					235					240	
act	gac	cat	tgt	gtt	aat	tgg	tat	aat	gtt	gga	tta	aat	ggt	tta	aga	768
Thr	Asp	His	Cys	Val	Asn	Trp	Tyr	Asn	Val	Gly	Leu	Asn	Gly	Leu	Arg	
				245					250					255		
ggt	tca	act	tat	gat	gca	tgg	gtc	aaa	ttt	aac	cgt	ttt	cgc	aga	gaa	816
Gly	Ser	Thr	Tyr	Asp	Ala	Trp	Val	Lys	Phe	Asn	Arg	Phe	Arg	Arg	Glu	
			260					265					270			
atg	act	tta	act	gta	tta	gat	cta	att	gta	ctt	ttc	cca	ttt	tat	gat	864
Met	Thr	Leu	Thr	Val	Leu	Asp	Leu	Ile	Val	Leu	Phe	Pro	Phe	Tyr	Asp	
		275					280					285				
att	cgg	tta	tac	tca	aaa	ggg	gtt	aaa	aca	gaa	cta	aca	aga	gac	att	912
Ile	Arg	Leu	Tyr	Ser	Lys	Gly	Val	Lys	Thr	Glu	Leu	Thr	Arg	Asp	Ile	
	290					295					300					
ttt	acg	gat	cca	att	ttt	tcc	ctc	gtt	aac	cta	atg	gtg	tac	gga	cca	960
Phe	Thr	Asp	Pro	Ile	Phe	Ser	Leu	Val	Asn	Leu	Met	Val	Tyr	Gly	Pro	
305					310					315					320	
act	ttt	ttg	agt	ata	gaa	aac	tct	att	cga	aaa	cct	cat	tta	ttt	gat	1008
Thr	Phe	Leu	Ser	Ile	Glu	Asn	Ser	Ile	Arg	Lys	Pro	His	Leu	Phe	Asp	
				325					330					335		
tat	tta	cag	ggg	att	gaa	ttt	cat	acg	cgt	ctt	caa	cct	ggt	tac	ttt	1056
Tyr	Leu	Gln	Gly	Ile	Glu	Phe	His	Thr	Arg	Leu	Gln	Pro	Gly	Tyr	Phe	
			340					345					350			
ggg	aaa	gat	tct	ttc	aat	tat	tgg	tct	ggt	aat	tat	gta	gaa	act	aga	1104
Gly	Lys	Asp	Ser	Phe	Asn	Tyr	Trp	Ser	Gly	Asn	Tyr	Val	Glu	Thr	Arg	
		355					360					365				
cct	agt	ata	gga	tct	agt	aag	aca	att	act	tcc	cca	ttt	tat	gga	gat	1152
Pro	Ser	Ile	Gly	Ser	Ser	Lys	Thr	Ile	Thr	Ser	Pro	Phe	Tyr	Gly	Asp	
		370				375					380					
aaa	tct	act	gaa	cct	gta	caa	aag	cta	agc	ttt	gat	gga	caa	aaa	gtt	1200
Lys	Ser	Thr	Glu	Pro	Val	Gln	Lys	Leu	Ser	Phe	Asp	Gly	Gln	Lys	Val	
385					390					395					400	
tat	cga	act	ata	gct	aat	aca	gac	gta	gcg	gct	tgg	ccg	aat	ggt	aag	1248
Tyr	Arg	Thr	Ile	Ala	Asn	Thr	Asp	Val	Ala	Ala	Trp	Pro	Asn	Gly	Lys	
				405					410					415		
gta	tat	tta	ggt	gtt	acg	aaa	gtt	gat	ttt	agt	caa	tat	gat	gat	caa	1296
Val	Tyr	Leu	Gly	Val	Thr	Lys	Val	Asp	Phe	Ser	Gln	Tyr	Asp	Asp	Gln	
			420					425					430			
aaa	aat	gaa	act	agt	aca	caa	aca	tat	gat	tca	aaa	aga	aac	aat	ggc	1344
Lys	Asn	Glu	Thr	Ser	Thr	Gln	Thr	Tyr	Asp	Ser	Lys	Arg	Asn	Asn	Gly	
		435					440					445				
cat	gta	agt	gca	cag	gat	tct	att	gac	caa	tta	ccg	cca	gaa	aca	aca	1392
His	Val	Ser	Ala	Gln	Asp	Ser	Ile	Asp	Gln	Leu	Pro	Pro	Glu	Thr	Thr	

450	455	460	
gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa			1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu			
465	470	475	480
tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg			1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp			
	485	490	495
aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att			1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile			
	500	505	510
act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc			1584
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser			
	515	520	525
att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa			1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys			
	530	535	540
gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca			1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala			
545	550	555	560
gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act			1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr			
	565	570	575
aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc			1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile			
	580	585	590
tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca			1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr			
	595	600	605
ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag			1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys			
610	615	620	
aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc			1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile			
625	630	635	640
tat ata gat aag ata gaa ttt atc cca gta caa ttg taa			1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu			
	645	650	

<210> 36  
 <211> 652  
 <212> PRT  
 <213> Artificial sequence  
  
 <220>

<223> Recombinant delta endotoxin

<400> 36

Met	Asn	Pro	Asn	Asn	Arg	Ser	Glu	His	Asp	Thr	Ile	Lys	Val	Thr	Pro	
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Asn	Ser	Glu	Leu	Gln	Thr	Asn	His	Asn	Gln	Tyr	Pro	Leu	Ala	Asp	Asn	
			20					25					30			
Pro	Asn	Ser	Thr	Leu	Glu	Glu	Leu	Asn	Tyr	Lys	Glu	Phe	Leu	Arg	Met	
		35					40					45				
Thr	Glu	Asp	Ser	Ser	Thr	Glu	Val	Leu	Asp	Asn	Ser	Thr	Val	Lys	Asp	
	50					55					60					
Ala	Val	Gly	Thr	Gly	Ile	Ser	Val	Val	Gly	Gln	Ile	Leu	Gly	Val	Val	
65					70					75					80	
Gly	Val	Pro	Phe	Ala	Gly	Ala	Leu	Thr	Ser	Phe	Tyr	Gln	Ser	Phe	Leu	
				85					90					95		
Asn	Thr	Ile	Trp	Pro	Ser	Asp	Ala	Asp	Pro	Trp	Lys	Ala	Phe	Met	Ala	
			100					105					110			
Gln	Val	Glu	Val	Leu	Ile	Asp	Lys	Lys	Ile	Glu	Glu	Tyr	Ala	Lys	Ser	
		115					120					125				
Lys	Ala	Leu	Ala	Glu	Leu	Gln	Gly	Leu	Gln	Asn	Asn	Phe	Glu	Asp	Tyr	
	130					135					140					
Val	Asn	Ala	Leu	Asn	Ser	Trp	Lys	Lys	Thr	Pro	Leu	Ser	Leu	Arg	Ser	
145					150					155					160	
Lys	Arg	Ser	Gln	Asp	Arg	Ile	Arg	Glu	Leu	Phe	Ser	Gln	Ala	Glu	Ser	
				165					170					175		
His	Phe	Arg	Asn	Ser	Met	Pro	Ser	Phe	Ala	Val	Ser	Lys	Phe	Glu	Val	
			180					185					190			
Leu	Phe	Leu	Pro	Thr	Tyr	Ala	Gln	Ala	Ala	Asn	Thr	His	Leu	Leu	Leu	
		195					200					205				
Leu	Lys	Asp	Ala	Gln	Val	Phe	Gly	Glu	Glu	Trp	Gly	Tyr	Ser	Ser	Glu	
	210					215					220					
Asp	Val	Ala	Glu	Phe	Tyr	His	Arg	Gln	Leu	Lys	Leu	Thr	Gln	Gln	Tyr	
225					230					235					240	
Thr	Asp	His	Cys	Val	Asn	Trp	Tyr	Asn	Val	Gly	Leu	Asn	Gly	Leu	Arg	
			245						250					255		
Gly	Ser	Thr	Tyr	Asp	Ala	Trp	Val	Lys	Phe	Asn	Arg	Phe	Arg	Arg	Glu	
			260					265					270			
Met	Thr	Leu	Thr	Val	Leu	Asp	Leu	Ile	Val	Leu	Phe	Pro	Phe	Tyr	Asp	
		275					280					285				

Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile  
 290 295 300  
 Phe Thr Asp Pro Ile Phe Ser Leu Val Asn Leu Met Val Tyr Gly Pro  
 305 310 315 320  
 Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp  
 325 330 335  
 Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe  
 340 345 350  
 Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg  
 355 360 365  
 Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp  
 370 375 380  
 Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val  
 385 390 395 400  
 Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys  
 405 410 415  
 Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln  
 420 425 430  
 Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly  
 435 440 445  
 His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr  
 450 455 460  
 Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu  
 465 470 475 480  
 Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp  
 485 490 495  
 Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile  
 500 505 510  
 Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser  
 515 520 525  
 Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys  
 530 535 540  
 Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala  
 545 550 555 560  
 Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr  
 565 570 575  
 Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile  
 580 585 590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr  
 595 600 605  
 Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys  
 610 615 620  
 Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile  
 625 630 635 640  
 Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu  
 645 650

<210> 37  
 <211> 1959  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Recombinant delta endotoxin

<220>  
 <221> CDS  
 <222> (1)..(1956)

<400> 37  
 atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct 48  
 Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro  
 1 5 10 15  
 aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat 96  
 Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn  
 20 25 30  
 cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg 144  
 Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met  
 35 40 45  
 act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat 192  
 Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp  
 50 55 60  
 gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta 240  
 Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val  
 65 70 75 80  
 gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt 288  
 Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu  
 85 90 95  
 aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca 336  
 Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala  
 100 105 110  
 caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt 384



Gln	Val	Glu	Val	Leu	Ile	Asp	Lys	Lys	Ile	Glu	Glu	Tyr	Ala	Lys	Ser		
		115					120					125					
aaa	gct	ctt	gca	gag	tta	cag	ggc	ctt	caa	aat	aat	ttc	gaa	gat	tat		432
Lys	Ala	Leu	Ala	Glu	Leu	Gln	Gly	Leu	Gln	Asn	Asn	Phe	Glu	Asp	Tyr		
		130				135					140						
ggt	aat	gcg	tta	aat	tcc	tgg	aag	aaa	aca	cct	tta	agt	ttg	cga	agt		480
Val	Asn	Ala	Leu	Asn	Ser	Trp	Lys	Lys	Thr	Pro	Leu	Ser	Leu	Arg	Ser		
					150					155					160		
aaa	aga	agc	caa	gat	cga	ata	agg	gaa	ctt	ttt	tct	caa	gca	gaa	agt		528
Lys	Arg	Ser	Gln	Asp	Arg	Ile	Arg	Glu	Leu	Phe	Ser	Gln	Ala	Glu	Ser		
				165					170					175			
cat	ttt	cgt	aat	tcc	atg	ccg	tca	ttt	gca	gtt	tcc	aaa	ttc	gaa	gtg		576
His	Phe	Arg	Asn	Ser	Met	Pro	Ser	Phe	Ala	Val	Ser	Lys	Phe	Glu	Val		
			180					185					190				
ctg	ttt	cta	cca	aca	tat	gca	caa	gct	gca	aat	aca	cat	tta	ttg	cta		624
Leu	Phe	Leu	Pro	Thr	Tyr	Ala	Gln	Ala	Ala	Asn	Thr	His	Leu	Leu	Leu		
		195					200					205					
tta	aaa	gat	gct	caa	gtt	ttt	gga	gaa	gaa	tgg	gga	tat	tct	tca	gaa		672
Leu	Lys	Asp	Ala	Gln	Val	Phe	Gly	Glu	Glu	Trp	Gly	Tyr	Ser	Ser	Glu		
	210					215					220						
gat	gtt	gct	gaa	ttt	tat	cat	aga	caa	tta	aaa	ctt	aca	caa	caa	tac		720
Asp	Val	Ala	Glu	Phe	Tyr	His	Arg	Gln	Leu	Lys	Leu	Thr	Gln	Gln	Tyr		
					230					235					240		
act	gac	cat	tgt	gtt	aat	tgg	tat	aat	gtt	gga	tta	aat	ggt	tta	aga		768
Thr	Asp	His	Cys	Val	Asn	Trp	Tyr	Asn	Val	Gly	Leu	Asn	Gly	Leu	Arg		
				245				250						255			
ggt	tca	act	tat	gat	gca	tgg	gtc	aaa	ttt	aac	cgt	ttt	cgc	aga	gaa		816
Gly	Ser	Thr	Tyr	Asp	Ala	Trp	Val	Lys	Phe	Asn	Arg	Phe	Arg	Arg	Glu		
			260					265					270				
atg	act	tta	act	gta	tta	gat	cta	att	gta	ctt	ttc	cca	ttt	tat	gat		864
Met	Thr	Leu	Thr	Val	Leu	Asp	Leu	Ile	Val	Leu	Phe	Pro	Phe	Tyr	Asp		
		275					280					285					
att	cgg	tta	tac	tca	aaa	ggg	gtt	aaa	aca	gaa	cta	aca	aga	gac	att		912
Ile	Arg	Leu	Tyr	Ser	Lys	Gly	Val	Lys	Thr	Glu	Leu	Thr	Arg	Asp	Ile		
		290				295					300						
ttt	acg	gat	cca	att	ttt	tct	ctt	agg	aca	cca	ctt	gcg	tac	gga	cca		960
Phe	Thr	Asp	Pro	Ile	Phe	Ser	Leu	Arg	Thr	Pro	Leu	Ala	Tyr	Gly	Pro		
		305			310					315					320		
act	ttt	ttg	agt	ata	gaa	aac	tct	att	cga	aaa	cct	cat	tta	ttt	gat		1008
Thr	Phe	Leu	Ser	Ile	Glu	Asn	Ser	Ile	Arg	Lys	Pro	His	Leu	Phe	Asp		
				325					330					335			
tat	tta	cag	ggg	att	gaa	ttt	cat	acg	cgt	ctt	caa	cct	ggt	tac	ttt		1056
Tyr	Leu	Gln	Gly	Ile	Glu	Phe	His	Thr	Arg	Leu	Gln	Pro	Gly	Tyr	Phe		

340	345	350	
ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg 355 360 365			1104
cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp 370 375 380			1152
aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val 385 390 395 400			1200
tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys 405 410 415			1248
gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln 420 425 430			1296
aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly 435 440 445			1344
cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr 450 455 460			1392
gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu 465 470 475 480			1440
tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp 485 490 495			1488
aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile 500 505 510			1536
act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser 515 520 525			1584
att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys 530 535 540			1632
gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala 545 550 555 560			1680
gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr 565 570 575			1728

aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc	1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile	
580 585 590	
tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca	1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr	
595 600 605	
ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag	1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys	
610 615 620	
aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc	1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile	
625 630 635 640	
tat ata gat aag ata gaa ttt atc cca gta caa ttg taa	1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu	
645 650	

<210> 38  
 <211> 652  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Recombinant delta endotoxin

<400> 38

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Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn	
20 25 30	
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met	
35 40 45	
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp	
50 55 60	
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val	
65 70 75 80	
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu	
85 90 95	
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala	
100 105 110	
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser	
115 120 125	
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr	

130	135	140
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser		
145	150	155 160
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser		
	165	170 175
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val		
	180	185 190
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu		
	195	200 205
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu		
	210	215 220
Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr		
225	230	235 240
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg		
	245	250 255
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu		
	260	265 270
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp		
	275	280 285
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile		
	290	295 300
Phe Thr Asp Pro Ile Phe Ser Leu Arg Thr Pro Leu Ala Tyr Gly Pro		
305	310	315 320
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp		
	325	330 335
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe		
	340	345 350
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg		
	355	360 365
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp		
	370	375 380
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val		
385	390	395 400
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys		
	405	410 415
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln		
	420	425 430
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly		

435		440		445
His Val Ser Ala Gln Asp	Ser Ile Asp Gln Leu Pro	Pro Glu Thr Thr		
450	455	460		
Asp Glu Pro Leu Glu Lys	Ala Tyr Ser His Gln Leu	Asn Tyr Ala Glu		
465	470	475	480	
Cys Phe Leu Met Gln Asp	Arg Arg Gly Thr Ile	Pro Phe Phe Thr Trp		
	485	490	495	
Thr His Arg Ser Val Asp	Phe Phe Asn Thr Ile	Asp Ala Glu Lys Ile		
	500	505	510	
Thr Gln Leu Pro Val Val	Lys Ala Tyr Ala Leu	Ser Ser Gly Ala Ser		
	515	520	525	
Ile Ile Glu Gly Pro Gly	Phe Thr Gly Gly Asn Leu	Leu Phe Leu Lys		
	530	535	540	
Glu Ser Ser Asn Ser Ile	Ala Lys Phe Lys Val Thr	Leu Asn Ser Ala		
545	550	555	560	
Ala Leu Leu Gln Arg Tyr	Arg Val Arg Ile Arg	Tyr Ala Ser Thr Thr		
	565	570	575	
Asn Leu Arg Leu Phe Val	Gln Asn Ser Asn Asn	Asp Phe Leu Val Ile		
	580	585	590	
Tyr Ile Asn Lys Thr Met	Asn Lys Asp Asp Asp	Leu Thr Tyr Gln Thr		
	595	600	605	
Phe Asp Leu Ala Thr Thr	Asn Ser Asn Met Gly	Phe Ser Gly Asp Lys		
	610	615	620	
Asn Glu Leu Ile Ile Gly	Ala Glu Ser Phe Val	Ser Asn Glu Lys Ile		
625	630	635	640	
Tyr Ile Asp Lys Ile Glu	Phe Ile Pro Val Gln	Leu		
	645	650		

<210> 39  
 <211> 1959  
 <212> DNA  
 <213> Artificial sequence  
 <220>  
 <223> Recombinant delta endotoxin

<220>  
 <221> CDS  
 <222> (1)..(1956)

<400> 39  
 atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct  
 Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro  
 1 5 10 15

48

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn 20 25 30	96
cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met 35 40 45	144
act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp 50 55 60	192
gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val 65 70 75 80	240
gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu 85 90 95	288
aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala 100 105 110	336
caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser 115 120 125	384
aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr 130 135 140	432
gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser 145 150 155 160	480
aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser 165 170 175	528
cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val 180 185 190	576
ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu 195 200 205	624
tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu 210 215 220	672
gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr 225 230 235 240	720

act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga	768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg	
245 250 255	
ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa	816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu	
260 265 270	
atg act tta act gta tta gat cta att gta ctt ttc cca ttt ttc aat	864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Phe Asn	
275 280 285	
att ttg ctt tac agt aaa ggg gtt aaa aca gaa cta aca aga gac att	912
Ile Leu Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile	
290 295 300	
ttt acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca	960
Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro	
305 310 315 320	
act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat	1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp	
325 330 335	
tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt	1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe	
340 345 350	
ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga	1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg	
355 360 365	
cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat	1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp	
370 375 380	
aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt	1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val	
385 390 395 400	
tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag	1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys	
405 410 415	
gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa	1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln	
420 425 430	
aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc	1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly	
435 440 445	
cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca	1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr	
450 455 460	
gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa	1440

Asp	Glu	Pro	Leu	Glu	Lys	Ala	Tyr	Ser	His	Gln	Leu	Asn	Tyr	Ala	Glu		
465					470					475					480		
tgt	ttc	tta	atg	cag	gac	cgt	cgt	gga	aca	att	cca	ttt	ttt	act	tgg	1488	
Cys	Phe	Leu	Met	Gln	Asp	Arg	Arg	Gly	Thr	Ile	Pro	Phe	Phe	Thr	Trp		
				485					490					495			
aca	cat	aga	agt	gta	gac	ttt	ttt	aat	aca	att	gat	gct	gaa	aag	att	1536	
Thr	His	Arg	Ser	Val	Asp	Phe	Phe	Asn	Thr	Ile	Asp	Ala	Glu	Lys	Ile		
			500					505					510				
act	caa	ctt	cca	gta	gtg	aaa	gca	tat	gcc	ttg	tct	tca	ggt	gct	tcc	1584	
Thr	Gln	Leu	Pro	Val	Val	Lys	Ala	Tyr	Ala	Leu	Ser	Ser	Gly	Ala	Ser		
		515					520					525					
att	att	gaa	ggt	cca	gga	ttc	aca	gga	gga	aat	tta	cta	ttc	cta	aaa	1632	
Ile	Ile	Glu	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Asn	Leu	Leu	Phe	Leu	Lys		
	530					535					540						
gaa	tct	agt	aat	tca	att	gct	aaa	ttt	aaa	gtt	aca	tta	aat	tca	gca	1680	
Glu	Ser	Ser	Asn	Ser	Ile	Ala	Lys	Phe	Lys	Val	Thr	Leu	Asn	Ser	Ala		
545					550					555					560		
gcc	ttg	tta	caa	cga	tat	cgt	gta	aga	ata	cgc	tat	gct	tct	acc	act	1728	
Ala	Leu	Leu	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg	Tyr	Ala	Ser	Thr	Thr		
				565					570					575			
aac	tta	cga	ctt	ttt	gtg	caa	aat	tca	aac	aat	gat	ttt	ctt	gtc	atc	1776	
Asn	Leu	Arg	Leu	Phe	Val	Gln	Asn	Ser	Asn	Asn	Asp	Phe	Leu	Val	Ile		
			580					585					590				
tac	att	aat	aaa	act	atg	aat	aaa	gat	gat	gat	tta	aca	tat	caa	aca	1824	
Tyr	Ile	Asn	Lys	Thr	Met	Asn	Lys	Asp	Asp	Asp	Leu	Thr	Tyr	Gln	Thr		
		595					600					605					
ttt	gat	ctc	gca	act	act	aat	tct	aat	atg	ggg	ttc	tcg	ggt	gat	aag	1872	
Phe	Asp	Leu	Ala	Thr	Thr	Asn	Ser	Asn	Met	Gly	Phe	Ser	Gly	Asp	Lys		
	610					615					620						
aat	gaa	ctt	ata	ata	gga	gca	gaa	tct	ttc	gtt	tct	aat	gaa	aaa	atc	1920	
Asn	Glu	Leu	Ile	Ile	Gly	Ala	Glu	Ser	Phe	Val	Ser	Asn	Glu	Lys	Ile		
625					630					635					640		
tat	ata	gat	aag	ata	gaa	ttt	atc	cca	gta	caa	ttg	taa				1959	
Tyr	Ile	Asp	Lys	Ile	Glu	Phe	Ile	Pro	Val	Gln	Leu						
				645					650								

<210> 40

<211> 652

<212> PRT

<213> Artificial sequence

<220>

<223> Recombinant delta endotoxin

<400> 40



Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro  
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 Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn  
 20 25 30  
 Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met  
 35 40 45  
 Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp  
 50 55 60  
 Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val  
 65 70 75 80  
 Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu  
 85 90 95  
 Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala  
 100 105 110  
 Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser  
 115 120 125  
 Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr  
 130 135 140  
 Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser  
 145 150 155 160  
 Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser  
 165 170 175  
 His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val  
 180 185 190  
 Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu  
 195 200 205  
 Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu  
 210 215 220  
 Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr  
 225 230 235 240  
 Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg  
 245 250 255  
 Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu  
 260 265 270  
 Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Phe Asn  
 275 280 285  
 Ile Leu Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile  
 290 295 300

Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro  
 305 310 315 320  
 Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp  
 325 330 335  
 Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe  
 340 345 350  
 Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg  
 355 360 365  
 Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp  
 370 375 380  
 Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val  
 385 390 395 400  
 Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys  
 405 410 415  
 Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln  
 420 425 430  
 Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly  
 435 440 445  
 His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr  
 450 455 460  
 Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu  
 465 470 475 480  
 Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp  
 485 490 495  
 Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile  
 500 505 510  
 Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser  
 515 520 525  
 Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys  
 530 535 540  
 Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala  
 545 550 555 560  
 Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr  
 565 570 575  
 Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile  
 580 585 590  
 Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr  
 595 600 605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys  
610 615 620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile  
625 630 635 640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu  
645 650

<210> 41  
<211> 1959  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Recombinant delta endotoxin

<220>  
<221> CDS  
<222> (1)..(1956)

<400> 41  
atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct 48  
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro  
1 5 10 15

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat 96  
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn  
20 25 30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg 144  
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met  
35 40 45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat 192  
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp  
50 55 60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta 240  
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val  
65 70 75 80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt 288  
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu  
85 90 95

aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca 336  
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala  
100 105 110

caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt 384  
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser  
115 120 125

aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat	432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr	
130 135 140	
ggt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt	480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser	
145 150 155 160	
aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt	528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser	
165 170 175	
cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg	576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val	
180 185 190	
ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta	624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu	
195 200 205	
tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa	672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu	
210 215 220	
gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac	720
Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr	
225 230 235 240	
act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga	768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg	
245 250 255	
ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa	816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu	
260 265 270	
atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat	864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp	
275 280 285	
att gtg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att	912
Ile Val Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile	
290 295 300	
ttt acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca	960
Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro	
305 310 315 320	
act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat	1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp	
325 330 335	
tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt	1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe	
340 345 350	
ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga	1104

Gly	Lys	Asp	Ser	Phe	Asn	Tyr	Trp	Ser	Gly	Asn	Tyr	Val	Glu	Thr	Arg	
		355					360					365				
cct	agt	ata	gga	tct	agt	aag	aca	att	act	tcc	cca	ttt	tat	gga	gat	1152
Pro	Ser	Ile	Gly	Ser	Ser	Lys	Thr	Ile	Thr	Ser	Pro	Phe	Tyr	Gly	Asp	
	370					375					380					
aaa	tct	act	gaa	cct	gta	caa	aag	cta	agc	ttt	gat	gga	caa	aaa	gtt	1200
Lys	Ser	Thr	Glu	Pro	Val	Gln	Lys	Leu	Ser	Phe	Asp	Gly	Gln	Lys	Val	
385					390					395					400	
tat	cga	act	ata	gct	aat	aca	gac	gta	gcg	gct	tgg	ccg	aat	ggt	aag	1248
Tyr	Arg	Thr	Ile	Ala	Asn	Thr	Asp	Val	Ala	Ala	Trp	Pro	Asn	Gly	Lys	
				405					410					415		
gta	tat	tta	ggt	gtt	acg	aaa	gtt	gat	ttt	agt	caa	tat	gat	gat	caa	1296
Val	Tyr	Leu	Gly	Val	Thr	Lys	Val	Asp	Phe	Ser	Gln	Tyr	Asp	Asp	Gln	
			420					425					430			
aaa	aat	gaa	act	agt	aca	caa	aca	tat	gat	tca	aaa	aga	aac	aat	ggc	1344
Lys	Asn	Glu	Thr	Ser	Thr	Gln	Thr	Tyr	Asp	Ser	Lys	Arg	Asn	Asn	Gly	
		435					440					445				
cat	gta	agt	gca	cag	gat	tct	att	gac	caa	tta	ccg	cca	gaa	aca	aca	1392
His	Val	Ser	Ala	Gln	Asp	Ser	Ile	Asp	Gln	Leu	Pro	Pro	Glu	Thr	Thr	
	450					455					460					
gat	gaa	cca	ctt	gaa	aaa	gca	tat	agt	cat	cag	ctt	aat	tac	gcg	gaa	1440
Asp	Glu	Pro	Leu	Glu	Lys	Ala	Tyr	Ser	His	Gln	Leu	Asn	Tyr	Ala	Glu	
465					470					475					480	
tgt	ttc	tta	atg	cag	gac	cgt	cgt	gga	aca	att	cca	ttt	ttt	act	tgg	1488
Cys	Phe	Leu	Met	Gln	Asp	Arg	Arg	Gly	Thr	Ile	Pro	Phe	Phe	Thr	Trp	
				485				490						495		
aca	cat	aga	agt	gta	gac	ttt	ttt	aat	aca	att	gat	gct	gaa	aag	att	1536
Thr	His	Arg	Ser	Val	Asp	Phe	Phe	Asn	Thr	Ile	Asp	Ala	Glu	Lys	Ile	
			500					505					510			
act	caa	ctt	cca	gta	gtg	aaa	gca	tat	gcc	ttg	tct	tca	ggt	gct	tcc	1584
Thr	Gln	Leu	Pro	Val	Val	Lys	Ala	Tyr	Ala	Leu	Ser	Ser	Gly	Ala	Ser	
		515					520					525				
att	att	gaa	ggt	cca	gga	ttc	aca	gga	gga	aat	tta	cta	ttc	cta	aaa	1632
Ile	Ile	Glu	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Asn	Leu	Leu	Phe	Leu	Lys	
		530				535					540					
gaa	tct	agt	aat	tca	att	gct	aaa	ttt	aaa	gtt	aca	tta	aat	tca	gca	1680
Glu	Ser	Ser	Asn	Ser	Ile	Ala	Lys	Phe	Lys	Val	Thr	Leu	Asn	Ser	Ala	
545					550					555					560	
gcc	ttg	tta	caa	cga	tat	cgt	gta	aga	ata	cgc	tat	gct	tct	acc	act	1728
Ala	Leu	Leu	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg	Tyr	Ala	Ser	Thr	Thr	
				565					570					575		
aac	tta	cga	ctt	ttt	gtg	caa	aat	tca	aac	aat	gat	ttt	ctt	gtc	atc	1776
Asn	Leu	Arg	Leu	Phe	Val	Gln	Asn	Ser	Asn	Asn	Asp	Phe	Leu	Val	Ile	

	580	585	590	
tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca				1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr				
	595	600	605	
ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag				1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys				
	610	615	620	
aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc				1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile				
	625	630	635	640
tat ata gat aag ata gaa ttt atc cca gta caa ttg taa				1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu				
	645	650		

<210> 42  
 <211> 652  
 <212> PRT  
 <213> Artificial sequence  
  
 <220>  
 <223> Recombinant delta endotoxin  
  
 <400> 42

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro				
1 5 10 15				
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn				
20 25 30				
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met				
35 40 45				
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp				
50 55 60				
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val				
65 70 75 80				
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu				
85 90 95				
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala				
100 105 110				
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser				
115 120 125				
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr				
130 135 140				
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser				

145		150		155		160
Lys Arg Ser Gln Asp	Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser	165	170	175		
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val	180	185	190			
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu	195	200	205			
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu	210	215	220			
Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr	225	230	235	240		
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg	245	250	255			
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu	260	265	270			
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp	275	280	285			
Ile Val Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile	290	295	300			
Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro	305	310	315	320		
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp	325	330	335			
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe	340	345	350			
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg	355	360	365			
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp	370	375	380			
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val	385	390	395	400		
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys	405	410	415			
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln	420	425	430			
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly	435	440	445			
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr						

450		455		460
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu				
465		470		475
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp				
	485		490	495
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile				
	500		505	510
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser				
	515		520	525
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys				
	530		535	540
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala				
545		550		555
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr				
	565		570	575
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile				
	580		585	590
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr				
	595		600	605
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys				
	610		615	620
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile				
625		630		635
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu				
	645		650	

<210> 43  
 <211> 1959  
 <212> DNA  
 <213> Artificial sequence  
 <220>  
 <223> Recombinant delta endotoxin

<220>  
 <221> CDS  
 <222> (1)..(1956)

<400> 43	
atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct	48
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro	
1 5 10 15	
aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat	96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn	



20	25	30	
cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met 35 40 45			144
act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp 50 55 60			192
gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val 65 70 75 80			240
gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu 85 90 95			288
aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala 100 105 110			336
caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser 115 120 125			384
aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr 130 135 140			432
gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser 145 150 155 160			480
aaa aga agc caa ggt cga ata agg gaa ctt ttt tct caa gca gaa agt Lys Arg Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser 165 170 175			528
cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val 180 185 190			576
ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu 195 200 205			624
tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu 210 215 220			672
gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr 225 230 235 240			720
act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg 245 250 255			768

ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa	816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu	
260 265 270	
atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat	864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp	
275 280 285	
att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att	912
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile	
290 295 300	
ttt acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca	960
Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro	
305 310 315 320	
act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat	1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp	
325 330 335	
tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt	1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe	
340 345 350	
ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga	1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg	
355 360 365	
cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat	1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp	
370 375 380	
aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt	1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val	
385 390 395 400	
tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag	1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys	
405 410 415	
gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa	1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln	
420 425 430	
aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc	1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly	
435 440 445	
cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca	1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr	
450 455 460	
gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa	1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu	
465 470 475 480	

tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg	1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp	
485 490 495	
aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att	1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile	
500 505 510	
act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc	1584
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser	
515 520 525	
att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa	1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys	
530 535 540	
gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca	1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala	
545 550 555 560	
gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act	1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr	
565 570 575	
aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc	1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile	
580 585 590	
tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca	1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr	
595 600 605	
ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag	1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys	
610 615 620	
aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc	1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile	
625 630 635 640	
tat ata gat aag ata gaa ttt atc cca gta caa ttg taa	1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu	
645 650	

<210> 44

<211> 652

<212> PRT

<213> Artificial sequence

<220>

<223> Recombinant delta endotoxin

<400> 44

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1 5 10 15

Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn  
 20 25 30  
 Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met  
 35 40 45  
 Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp  
 50 55 60  
 Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val  
 65 70 75 80  
 Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu  
 85 90 95  
 Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala  
 100 105 110  
 Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser  
 115 120 125  
 Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr  
 130 135 140  
 Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser  
 145 150 155 160  
 Lys Arg Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser  
 165 170 175  
 His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val  
 180 185 190  
 Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu  
 195 200 205  
 Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu  
 210 215 220  
 Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr  
 225 230 235 240  
 Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg  
 245 250 255  
 Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu  
 260 265 270  
 Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp  
 275 280 285  
 Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile  
 290 295 300  
 Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro  
 305 310 315 320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp  
 325 330 335  
 Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe  
 340 345 350  
 Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg  
 355 360 365  
 Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp  
 370 375 380  
 Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val  
 385 390 395 400  
 Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys  
 405 410 415  
 Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln  
 420 425 430  
 Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly  
 435 440 445  
 His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr  
 450 455 460  
 Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu  
 465 470 475 480  
 Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp  
 485 490 495  
 Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile  
 500 505 510  
 Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser  
 515 520 525  
 Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys  
 530 535 540  
 Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala  
 545 550 555 560  
 Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr  
 565 570 575  
 Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile  
 580 585 590  
 Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr  
 595 600 605  
 Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys  
 610 615 620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile  
 625 630 635 640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu  
 645 650

<210> 45  
 <211> 1959  
 <212> DNA  
 <213> Artificial sequence  
 <220>  
 <223> Recombinant delta endotoxin

<220>  
 <221> CDS  
 <222> (1)..(1956)

<400> 45  
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 Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro  
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 aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat 96  
 Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn  
 20 25 30  
 cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg 144  
 Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met  
 35 40 45  
 act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat 192  
 Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp  
 50 55 60  
 gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta 240  
 Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val  
 65 70 75 80  
 gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt 288  
 Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu  
 85 90 95  
 aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca 336  
 Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala  
 100 105 110  
 caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt 384  
 Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser  
 115 120 125  
 aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat 432  
 Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr  
 130 135 140

gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga aat	480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Asn	
145 150 155 160	
cca cac agc caa ggt cga ata agg gaa ctt ttt tct caa gca gaa agt	528
Pro His Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser	
165 170 175	
cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg	576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val	
180 185 190	
ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta	624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu	
195 200 205	
tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa	672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu	
210 215 220	
gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac	720
Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr	
225 230 235 240	
act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga	768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg	
245 250 255	
ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa	816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu	
260 265 270	
atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat	864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp	
275 280 285	
att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att	912
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile	
290 295 300	
ttt acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca	960
Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro	
305 310 315 320	
act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat	1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp	
325 330 335	
tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt	1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe	
340 345 350	
ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga	1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg	
355 360 365	

cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp 370 375 380	1152
aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val 385 390 395 400	1200
tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys 405 410 415	1248
gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln 420 425 430	1296
aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly 435 440 445	1344
cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr 450 455 460	1392
gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu 465 470 475 480	1440
tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp 485 490 495	1488
aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile 500 505 510	1536
act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser 515 520 525	1584
att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys 530 535 540	1632
gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala 545 550 555 560	1680
gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr 565 570 575	1728
aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile 580 585 590	1776
tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca	1824



Tyr	Ile	Asn	Lys	Thr	Met	Asn	Lys	Asp	Asp	Asp	Leu	Thr	Tyr	Gln	Thr		
		595					600					605					
ttt	gat	ctc	gca	act	act	aat	tct	aat	atg	ggg	ttc	tcg	ggg	gat	aag		1872
Phe	Asp	Leu	Ala	Thr	Thr	Asn	Ser	Asn	Met	Gly	Phe	Ser	Gly	Asp	Lys		
	610					615				620							
aat	gaa	ctt	ata	ata	gga	gca	gaa	tct	ttc	gtt	tct	aat	gaa	aaa	atc		1920
Asn	Glu	Leu	Ile	Ile	Gly	Ala	Glu	Ser	Phe	Val	Ser	Asn	Glu	Lys	Ile		
	625				630					635					640		
tat	ata	gat	aag	ata	gaa	ttt	atc	cca	gta	caa	ttg	taa					1959
Tyr	Ile	Asp	Lys		Ile	Glu	Phe	Ile	Pro	Val	Gln	Leu					
					645					650							

<210> 46  
 <211> 652  
 <212> PRT  
 <213> Artificial sequence  
  
 <220>  
 <223> Recombinant delta endotoxin  
  
 <400> 46

Met	Asn	Pro	Asn	Asn	Arg	Ser	Glu	His	Asp	Thr	Ile	Lys	Val	Thr	Pro		
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Asn	Ser	Glu	Leu	Gln	Thr	Asn	His	Asn	Gln	Tyr	Pro	Leu	Ala	Asp	Asn		
		20					25						30				
Pro	Asn	Ser	Thr	Leu	Glu	Glu	Leu	Asn	Tyr	Lys	Glu	Phe	Leu	Arg	Met		
		35					40					45					
Thr	Glu	Asp	Ser	Ser	Thr	Glu	Val	Leu	Asp	Asn	Ser	Thr	Val	Lys	Asp		
	50					55				60							
Ala	Val	Gly	Thr	Gly	Ile	Ser	Val	Val	Gly	Gln	Ile	Leu	Gly	Val	Val		
	65				70					75					80		
Gly	Val	Pro	Phe	Ala	Gly	Ala	Leu	Thr	Ser	Phe	Tyr	Gln	Ser	Phe	Leu		
			85						90					95			
Asn	Thr	Ile	Trp	Pro	Ser	Asp	Ala	Asp	Pro	Trp	Lys	Ala	Phe	Met	Ala		
			100					105					110				
Gln	Val	Glu	Val	Leu	Ile	Asp	Lys	Lys	Ile	Glu	Glu	Tyr	Ala	Lys	Ser		
		115					120					125					
Lys	Ala	Leu	Ala	Glu	Leu	Gln	Gly	Leu	Gln	Asn	Asn	Phe	Glu	Asp	Tyr		
	130					135					140						
Val	Asn	Ala	Leu	Asn	Ser	Trp	Lys	Lys	Thr	Pro	Leu	Ser	Leu	Arg	Asn		
	145				150					155					160		
Pro	His	Ser	Gln	Gly	Arg	Ile	Arg	Glu	Leu	Phe	Ser	Gln	Ala	Glu	Ser		

H: 532973(BF8T01!.DOC)

465		470		475		480
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp						
		485		490		495
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile						
		500		505		510
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser						
		515		520		525
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys						
		530		535		540
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala						
		545		550		555
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr						
		565		570		575
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile						
		580		585		590
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr						
		595		600		605
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys						
		610		615		620
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile						
		625		630		635
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu						
		645		650		

<210> 47  
 <211> 1959  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Recombinant delta endotoxin

<220>  
 <221> CDS  
 <222> (1)..(1956)

<400> 47		
atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct		48
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1 5 10 15		
aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat		96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn		
20 25 30		

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met 35 40 45	144
act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp 50 55 60	192
gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val 65 70 75 80	240
gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu 85 90 95	288
aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala 100 105 110	336
caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser 115 120 125	384
aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr 130 135 140	432
gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser 145 150 155 160	480
aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser 165 170 175	528
cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val 180 185 190	576
ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu 195 200 205	624
tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu 210 215 220	672
gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr 225 230 235 240	720
act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg 245 250 255	768

ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa	816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu	
260 265 270	
atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat	864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp	
275 280 285	
gtt cgg tta tac cca aaa ggg gtt aaa aca gaa cta aca aga gac att	912
Val Arg Leu Tyr Pro Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile	
290 295 300	
ttt acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca	960
Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro	
305 310 315 320	
act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat	1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp	
325 330 335	
tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt	1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe	
340 345 350	
ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga	1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg	
355 360 365	
cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat	1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp	
370 375 380	
aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt	1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val	
385 390 395 400	
tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag	1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys	
405 410 415	
gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa	1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln	
420 425 430	
aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc	1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly	
435 440 445	
cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca	1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr	
450 455 460	
gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa	1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu	
465 470 475 480	
tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg	1488

Cys	Phe	Leu	Met	Gln	Asp	Arg	Arg	Gly	Thr	Ile	Pro	Phe	Phe	Thr	Trp	
				485					490					495		
aca	cat	aga	agt	gta	gac	ttt	ttt	aat	aca	att	gat	gct	gaa	aag	att	1536
Thr	His	Arg	Ser	Val	Asp	Phe	Phe	Asn	Thr	Ile	Asp	Ala	Glu	Lys	Ile	
			500					505					510			
act	caa	ctt	cca	gta	gtg	aaa	gca	tat	gcc	ttg	tct	tca	ggg	gct	tcc	1584
Thr	Gln	Leu	Pro	Val	Val	Lys	Ala	Tyr	Ala	Leu	Ser	Ser	Gly	Ala	Ser	
		515					520					525				
att	att	gaa	ggg	cca	gga	ttc	aca	gga	gga	aat	tta	cta	ttc	cta	aaa	1632
Ile	Ile	Glu	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Asn	Leu	Leu	Phe	Leu	Lys	
	530					535					540					
gaa	tct	agt	aat	tca	att	gct	aaa	ttt	aaa	gtt	aca	tta	aat	tca	gca	1680
Glu	Ser	Ser	Asn	Ser	Ile	Ala	Lys	Phe	Lys	Val	Thr	Leu	Asn	Ser	Ala	
545					550					555					560	
gcc	ttg	tta	caa	cga	tat	cgt	gta	aga	ata	cgc	tat	gct	tct	acc	act	1728
Ala	Leu	Leu	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg	Tyr	Ala	Ser	Thr	Thr	
			565						570					575		
aac	tta	cga	ctt	ttt	gtg	caa	aat	tca	aac	aat	gat	ttt	ctt	gtc	atc	1776
Asn	Leu	Arg	Leu	Phe	Val	Gln	Asn	Ser	Asn	Asn	Asp	Phe	Leu	Val	Ile	
			580					585					590			
tac	att	aat	aaa	act	atg	aat	aaa	gat	gat	gat	tta	aca	tat	caa	aca	1824
Tyr	Ile	Asn	Lys	Thr	Met	Asn	Lys	Asp	Asp	Asp	Leu	Thr	Tyr	Gln	Thr	
		595					600					605				
ttt	gat	ctc	gca	act	act	aat	tct	aat	atg	ggg	ttc	tcg	ggg	gat	aag	1872
Phe	Asp	Leu	Ala	Thr	Thr	Asn	Ser	Asn	Met	Gly	Phe	Ser	Gly	Asp	Lys	
	610					615					620					
aat	gaa	ctt	ata	ata	gga	gca	gaa	tct	ttc	gtt	tct	aat	gaa	aaa	atc	1920
Asn	Glu	Leu	Ile	Ile	Gly	Ala	Glu	Ser	Phe	Val	Ser	Asn	Glu	Lys	Ile	
625					630					635					640	
tat	ata	gat	aag	ata	gaa	ttt	atc	cca	gta	caa	ttg	taa				1959
Tyr	Ile	Asp	Lys	Ile	Glu	Phe	Ile	Pro	Val	Gln	Leu					
			645						650							

<210> 48

<211> 652

<212> PRT

<213> Artificial sequence

<220>

<223> Recombinant delta endotoxin

<400> 48

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 20 25 30  
 Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met  
 35 40 45  
 Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp  
 50 55 60  
 Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val  
 65 70 75 80  
 Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu  
 85 90 95  
 Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala  
 100 105 110  
 Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser  
 115 120 125  
 Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr  
 130 135 140  
 Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser  
 145 150 155 160  
 Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser  
 165 170 175  
 His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val  
 180 185 190  
 Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu  
 195 200 205  
 Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu  
 210 215 220  
 Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr  
 225 230 235 240  
 Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg  
 245 250 255  
 Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu  
 260 265 270  
 Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp  
 275 280 285  
 Val Arg Leu Tyr Pro Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile  
 290 295 300  
 Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro  
 305 310 315 320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp  
 325 330 335  
 Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe  
 340 345 350  
 Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg  
 355 360 365  
 Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp  
 370 375 380  
 Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val  
 385 390 395 400  
 Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys  
 405 410 415  
 Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln  
 420 425 430  
 Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly  
 435 440 445  
 His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr  
 450 455 460  
 Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu  
 465 470 475 480  
 Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp  
 485 490 495  
 Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile  
 500 505 510  
 Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser  
 515 520 525  
 Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys  
 530 535 540  
 Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala  
 545 550 555 560  
 Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr  
 565 570 575  
 Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile  
 580 585 590  
 Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr  
 595 600 605  
 Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys  
 610 615 620



Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile  
625 630 635 640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu  
645 650

<210> 49  
<211> 1959  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Recombinant delta endotoxin

<220>  
<221> CDS  
<222> (1)..(1956) .

<400> 49  
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aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat 96  
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn  
20 25 30  
  
cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg 144  
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met  
35 40 45  
  
act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat 192  
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp  
50 55 60  
  
gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta 240  
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val  
65 70 75 80  
  
gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt 288  
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu  
85 90 95  
  
aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca 336  
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala  
100 105 110  
  
caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt 384  
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser  
115 120 125  
  
aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat 432  
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr  
130 135 140

gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga aat	480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Asn	
145 150 155 160	
cca cac agc caa ggt cga ata agg gaa ctt ttt tct caa gca gaa agt	528
Pro His Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser	
165 170 175	
cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg	576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val	
180 185 190	
ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta	624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu	
195 200 205	
tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa	672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu	
210 215 220	
gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac	720
Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr	
225 230 235 240	
act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga	768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg	
245 250 255	
ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa	816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu	
260 265 270	
atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat	864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp	
275 280 285	
gtt cgg tta tac cca aaa ggg gtt aaa aca gaa cta aca aga gac att	912
Val Arg Leu Tyr Pro Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile	
290 295 300	
ttt acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca	960
Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro	
305 310 315 320	
act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat	1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp	
325 330 335	
tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt	1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe	
340 345 350	
ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga	1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg	
355 360 365	
cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat	1152

Pro	Ser	Ile	Gly	Ser	Ser	Lys	Thr	Ile	Thr	Ser	Pro	Phe	Tyr	Gly	Asp		
370						375					380						
aaa	tct	act	gaa	cct	gta	caa	aag	cta	agc	ttt	gat	gga	caa	aaa	gtt	1200	
Lys	Ser	Thr	Glu	Pro	Val	Gln	Lys	Leu	Ser	Phe	Asp	Gly	Gln	Lys	Val		
385					390					395					400		
tat	cga	act	ata	gct	aat	aca	gac	gta	gcg	gct	tgg	ccg	aat	ggg	aag	1248	
Tyr	Arg	Thr	Ile	Ala	Asn	Thr	Asp	Val	Ala	Ala	Trp	Pro	Asn	Gly	Lys		
				405					410					415			
gta	tat	tta	ggg	gtt	acg	aaa	gtt	gat	ttt	agt	caa	tat	gat	gat	caa	1296	
Val	Tyr	Leu	Gly	Val	Thr	Lys	Val	Asp	Phe	Ser	Gln	Tyr	Asp	Asp	Gln		
			420					425					430				
aaa	aat	gaa	act	agt	aca	caa	aca	tat	gat	tca	aaa	aga	aac	aat	ggc	1344	
Lys	Asn	Glu	Thr	Ser	Thr	Gln	Thr	Tyr	Asp	Ser	Lys	Arg	Asn	Asn	Gly		
		435					440					445					
cat	gta	agt	gca	cag	gat	tct	att	gac	caa	tta	ccg	cca	gaa	aca	aca	1392	
His	Val	Ser	Ala	Gln	Asp	Ser	Ile	Asp	Gln	Leu	Pro	Pro	Glu	Thr	Thr		
	450					455					460						
gat	gaa	cca	ctt	gaa	aaa	gca	tat	agt	cat	cag	ctt	aat	tac	gcg	gaa	1440	
Asp	Glu	Pro	Leu	Glu	Lys	Ala	Tyr	Ser	His	Gln	Leu	Asn	Tyr	Ala	Glu		
465					470					475					480		
tgt	ttc	tta	atg	cag	gac	cgt	cgt	gga	aca	att	cca	ttt	ttt	act	tgg	1488	
Cys	Phe	Leu	Met	Gln	Asp	Arg	Arg	Gly	Thr	Ile	Pro	Phe	Phe	Thr	Trp		
				485				490						495			
aca	cat	aga	agt	gta	gac	ttt	ttt	aat	aca	att	gat	gct	gaa	aag	att	1536	
Thr	His	Arg	Ser	Val	Asp	Phe	Phe	Asn	Thr	Ile	Asp	Ala	Glu	Lys	Ile		
			500					505					510				
act	caa	ctt	cca	gta	gtg	aaa	gca	tat	gcc	ttg	tct	tca	ggg	gct	tcc	1584	
Thr	Gln	Leu	Pro	Val	Val	Lys	Ala	Tyr	Ala	Leu	Ser	Ser	Gly	Ala	Ser		
		515					520					525					
att	att	gaa	ggg	cca	gga	ttc	aca	gga	gga	aat	tta	cta	ttc	cta	aaa	1632	
Ile	Ile	Glu	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Asn	Leu	Leu	Phe	Leu	Lys		
	530					535					540						
gaa	tct	agt	aat	tca	att	gct	aaa	ttt	aaa	gtt	aca	tta	aat	tca	gca	1680	
Glu	Ser	Ser	Asn	Ser	Ile	Ala	Lys	Phe	Lys	Val	Thr	Leu	Asn	Ser	Ala		
545					550					555					560		
gcc	ttg	tta	caa	cga	tat	cgt	gta	aga	ata	cgc	tat	gct	tct	acc	act	1728	
Ala	Leu	Leu	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg	Tyr	Ala	Ser	Thr	Thr		
				565					570					575			
aac	tta	cga	ctt	ttt	gtg	caa	aat	tca	aac	aat	gat	ttt	ctt	gtc	atc	1776	
Asn	Leu	Arg	Leu	Phe	Val	Gln	Asn	Ser	Asn	Asn	Asp	Phe	Leu	Val	Ile		
			580					585					590				
tac	att	aat	aaa	act	atg	aat	aaa	gat	gat	gat	tta	aca	tat	caa	aca	1824	
Tyr	Ile	Asn	Lys	Thr	Met	Asn	Lys	Asp	Asp	Asp	Leu	Thr	Tyr	Gln	Thr		

595	600	605	
ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag			1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys			
610	615	620	
aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc			1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile			
625	630	635	640
tat ata gat aag ata gaa ttt atc cca gta caa ttg taa			1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu			
645	650		

<210> 50  
 <211> 652  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Recombinant delta endotoxin

<400> 50

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Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn			
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Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met			
35	40	45	
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp			
50	55	60	
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val			
65	70	75	80
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu			
85	90	95	
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala			
100	105	110	
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser			
115	120	125	
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr			
130	135	140	
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Asn			
145	150	155	160
Pro His Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser			
165	170	175	

His	Phe	Arg	Asn	Ser	Met	Pro	Ser	Phe	Ala	Val	Ser	Lys	Phe	Glu	Val	180	185	190	
Leu	Phe	Leu	Pro	Thr	Tyr	Ala	Gln	Ala	Ala	Asn	Thr	His	Leu	Leu	Leu	195	200	205	
Leu	Lys	Asp	Ala	Gln	Val	Phe	Gly	Glu	Glu	Trp	Gly	Tyr	Ser	Ser	Glu	210	215	220	
Asp	Val	Ala	Glu	Phe	Tyr	His	Arg	Gln	Leu	Lys	Leu	Thr	Gln	Gln	Tyr	225	230	235	240
Thr	Asp	His	Cys	Val	Asn	Trp	Tyr	Asn	Val	Gly	Leu	Asn	Gly	Leu	Arg	245	250	255	
Gly	Ser	Thr	Tyr	Asp	Ala	Trp	Val	Lys	Phe	Asn	Arg	Phe	Arg	Arg	Glu	260	265	270	
Met	Thr	Leu	Thr	Val	Leu	Asp	Leu	Ile	Val	Leu	Phe	Pro	Phe	Tyr	Asp	275	280	285	
Val	Arg	Leu	Tyr	Pro	Lys	Gly	Val	Lys	Thr	Glu	Leu	Thr	Arg	Asp	Ile	290	295	300	
Phe	Thr	Asp	Pro	Ile	Phe	Ser	Leu	Asn	Thr	Leu	Gln	Glu	Tyr	Gly	Pro	305	310	315	320
Thr	Phe	Leu	Ser	Ile	Glu	Asn	Ser	Ile	Arg	Lys	Pro	His	Leu	Phe	Asp	325	330	335	
Tyr	Leu	Gln	Gly	Ile	Glu	Phe	His	Thr	Arg	Leu	Gln	Pro	Gly	Tyr	Phe	340	345	350	
Gly	Lys	Asp	Ser	Phe	Asn	Tyr	Trp	Ser	Gly	Asn	Tyr	Val	Glu	Thr	Arg	355	360	365	
Pro	Ser	Ile	Gly	Ser	Ser	Lys	Thr	Ile	Thr	Ser	Pro	Phe	Tyr	Gly	Asp	370	375	380	
Lys	Ser	Thr	Glu	Pro	Val	Gln	Lys	Leu	Ser	Phe	Asp	Gly	Gln	Lys	Val	385	390	395	400
Tyr	Arg	Thr	Ile	Ala	Asn	Thr	Asp	Val	Ala	Ala	Trp	Pro	Asn	Gly	Lys	405	410	415	
Val	Tyr	Leu	Gly	Val	Thr	Lys	Val	Asp	Phe	Ser	Gln	Tyr	Asp	Asp	Gln	420	425	430	
Lys	Asn	Glu	Thr	Ser	Thr	Gln	Thr	Tyr	Asp	Ser	Lys	Arg	Asn	Asn	Gly	435	440	445	
His	Val	Ser	Ala	Gln	Asp	Ser	Ile	Asp	Gln	Leu	Pro	Pro	Glu	Thr	Thr	450	455	460	
Asp	Glu	Pro	Leu	Glu	Lys	Ala	Tyr	Ser	His	Gln	Leu	Asn	Tyr	Ala	Glu	465	470	475	480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp  
 485 490 495  
 Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile  
 500 505 510  
 Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser  
 515 520 525  
 Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys  
 530 535 540  
 Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala  
 545 550 555 560  
 Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr  
 565 570 575  
 Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile  
 580 585 590  
 Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr  
 595 600 605  
 Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys  
 610 615 620  
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 Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu  
 645 650

<210> 51  
 <211> 1956  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Recombinant delta endotoxin

<220>  
 <221> CDS  
 <222> (1)..(1953)

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 aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat 96  
 Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn  
 20 25 30  
 cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg 144

Pro	Asn	Ser	Thr	Leu	Glu	Glu	Leu	Asn	Tyr	Lys	Glu	Phe	Leu	Arg	Met		
		35					40					45					
act	gaa	gac	agt	tct	acg	gaa	gtg	cta	gac	aac	tct	aca	gta	aaa	gat	192	
Thr	Glu	Asp	Ser	Ser	Thr	Glu	Val	Leu	Asp	Asn	Ser	Thr	Val	Lys	Asp		
	50					55				60							
gca	gtt	ggg	aca	gga	att	tct	gtt	gta	ggg	cag	att	tta	ggt	gtt	gta	240	
Ala	Val	Gly	Thr	Gly	Ile	Ser	Val	Val	Gly	Gln	Ile	Leu	Gly	Val	Val		
65					70					75					80		
gga	gtt	cca	ttt	gct	ggg	gca	ctc	act	tca	ttt	tat	caa	tca	ttt	ctt	288	
Gly	Val	Pro	Phe	Ala	Gly	Ala	Leu	Thr	Ser	Phe	Tyr	Gln	Ser	Phe	Leu		
				85					90					95			
aac	act	ata	tgg	cca	agt	gaa	gac	cca	tgg	aag	gct	ttt	atg	gca	caa	336	
Asn	Thr	Ile	Trp	Pro	Ser	Glu	Asp	Pro	Trp	Lys	Ala	Phe	Met	Ala	Gln		
			100					105					110				
gtt	gaa	gta	ctg	ata	gat	aag	aaa	ata	gag	gag	tat	gct	aaa	agt	aaa	384	
Val	Glu	Val	Leu	Ile	Asp	Lys	Lys	Ile	Glu	Glu	Tyr	Ala	Lys	Ser	Lys		
		115					120					125					
gct	ctt	gca	gag	tta	cag	ggg	ctt	caa	aat	aat	ttc	gaa	gat	tat	gtt	432	
Ala	Leu	Ala	Glu	Leu	Gln	Gly	Leu	Gln	Asn	Asn	Phe	Glu	Asp	Tyr	Val		
	130					135					140						
aat	gcg	tta	aat	tcc	tgg	aag	aaa	aca	cct	tta	agt	ttg	cga	agt	aaa	480	
Asn	Ala	Leu	Asn	Ser	Trp	Lys	Lys	Thr	Pro	Leu	Ser	Leu	Arg	Ser	Lys		
145					150					155					160		
aga	agc	caa	gat	cga	ata	agg	gaa	ctt	ttt	tct	caa	gca	gaa	agt	cat	528	
Arg	Ser	Gln	Asp	Arg	Ile	Arg	Glu	Leu	Phe	Ser	Gln	Ala	Glu	Ser	His		
				165					170					175			
ttt	cgt	aat	tcc	atg	ccg	tca	ttt	gca	gtt	tcc	aaa	ttc	gaa	gtg	ctg	576	
Phe	Arg	Asn	Ser	Met	Pro	Ser	Phe	Ala	Val	Ser	Lys	Phe	Glu	Val	Leu		
			180					185					190				
ttt	cta	cca	aca	tat	gca	caa	gct	gca	aat	aca	cat	tta	ttg	cta	tta	624	
Phe	Leu	Pro	Thr	Tyr	Ala	Gln	Ala	Ala	Asn	Thr	His	Leu	Leu	Leu	Leu		
		195					200					205					
aaa	gat	gct	caa	gtt	ttt	gga	gaa	gaa	tgg	gga	tat	tct	tca	gaa	gat	672	
Lys	Asp	Ala	Gln	Val	Phe	Gly	Glu	Glu	Trp	Gly	Tyr	Ser	Ser	Glu	Asp		
	210					215				220							
gtt	gct	gaa	ttt	tat	cat	aga	caa	tta	aaa	ctt	aca	caa	caa	tac	act	720	
Val	Ala	Glu	Phe	Tyr	His	Arg	Gln	Leu	Lys	Leu	Thr	Gln	Gln	Tyr	Thr		
225					230					235					240		
gac	cat	tgt	gtt	aat	tgg	tat	aat	gtt	gga	tta	aat	ggt	tta	aga	ggt	768	
Asp	His	Cys	Val	Asn	Trp	Tyr	Asn	Val	Gly	Leu	Asn	Gly	Leu	Arg	Gly		
				245					250					255			
tca	act	tat	gat	gca	tgg	gtc	aaa	ttt	aac	cgt	ttt	cgc	aga	gaa	atg	816	
Ser	Thr	Tyr	Asp	Ala	Trp	Val	Lys	Phe	Asn	Arg	Phe	Arg	Arg	Glu	Met		

260	265	270	
act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat att Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp Ile 275 280 285			864
cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att ttt Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile Phe 290 295 300			912
acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca act Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro Thr 305 310 315 320			960
ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat tat Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp Tyr 325 330 335			1008
tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt ggg Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe Gly 340 345 350			1056
aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga cct Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg Pro 355 360 365			1104
agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat aaa Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp Lys 370 375 380			1152
tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt tat Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val Tyr 385 390 395 400			1200
cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag gta Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys Val 405 410 415			1248
tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa aaa Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln Lys 420 425 430			1296
aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc cat Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly His 435 440 445			1344
gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca gat Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr Asp 450 455 460			1392
gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa tgt Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu Cys 465 470 475 480			1440
ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg aca Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp Thr 485 490 495			1488



cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att act	1536
His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile Thr	
500 505 510	
caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc att	1584
Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser Ile	
515 520 525	
att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa gaa	1632
Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys Glu	
530 535 540	
tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca gcc	1680
Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala Ala	
545 550 555 560	
ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act aac	1728
Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr Asn	
565 570 575	
tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc tac	1776
Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile Tyr	
580 585 590	
att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca ttt	1824
Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr Phe	
595 600 605	
gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag aat	1872
Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys Asn	
610 615 620	
gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc tat	1920
Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile Tyr	
625 630 635 640	
ata gat aag ata gaa ttt atc cca gta caa ttg taa	1956
Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu	
645 650	

<210> 52

<211> 651

<212> PRT

<213> Artificial sequence

<220>

<223> Recombinant delta endotoxin

<400> 52

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
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Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
20 25 30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met  
 35 40 45  
 Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp  
 50 55 60  
 Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val  
 65 70 75 80  
 Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu  
 85 90 95  
 Asn Thr Ile Trp Pro Ser Glu Asp Pro Trp Lys Ala Phe Met Ala Gln  
 100 105 110  
 Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser Lys  
 115 120 125  
 Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr Val  
 130 135 140  
 Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser Lys  
 145 150 155 160  
 Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser His  
 165 170 175  
 Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val Leu  
 180 185 190  
 Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu Leu  
 195 200 205  
 Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu Asp  
 210 215 220  
 Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr Thr  
 225 230 235 240  
 Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg Gly  
 245 250 255  
 Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu Met  
 260 265 270  
 Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp Ile  
 275 280 285  
 Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile Phe  
 290 295 300  
 Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro Thr  
 305 310 315 320  
 Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp Tyr  
 325 330 335

Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe Gly  
 340 345 350  
 Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg Pro  
 355 360 365  
 Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp Lys  
 370 375 380  
 Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val Tyr  
 385 390 395 400  
 Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys Val  
 405 410 415  
 Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln Lys  
 420 425 430  
 Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly His  
 435 440 445  
 Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr Asp  
 450 455 460  
 Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu Cys  
 465 470 475 480  
 Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp Thr  
 485 490 495  
 His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile Thr  
 500 505 510  
 Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser Ile  
 515 520 525  
 Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys Glu  
 530 535 540  
 Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala Ala  
 545 550 555 560  
 Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr Asn  
 565 570 575  
 Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile Tyr  
 580 585 590  
 Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr Phe  
 595 600 605  
 Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys Asn  
 610 615 620  
 Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile Tyr  
 625 630 635 640

Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu  
645 650

<210> 53  
<211> 1959  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Recombinant delta endotoxin

<220>  
<221> CDS  
<222> (1)..(1956)

<400> 53  
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Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro  
1 5 10 15  
  
aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat 96  
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn  
20 25 30  
  
cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg 144  
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met  
35 40 45  
  
act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat 192  
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp  
50 55 60  
  
gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta 240  
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val  
65 70 75 80  
  
gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt 288  
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu  
85 90 95  
  
aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca 336  
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala  
100 105 110  
  
caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt 384  
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser  
115 120 125  
  
aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat 432  
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr  
130 135 140  
  
gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt 480  
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser

145	150	155	160	
aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt				528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser	165	170	175	
cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc gga ttc gaa gtg				576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Gly Phe Glu Val	180	185	190	
ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta				624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu	195	200	205	
tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa				672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu	210	215	220	
gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac				720
Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr	225	230	235	240
act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga				768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg	245	250	255	
ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa				816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu	260	265	270	
atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat				864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp	275	280	285	
att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att				912
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile	290	295	300	
ttt acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca				960
Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro	305	310	315	320
act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat				1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp	325	330	335	
tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt				1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe	340	345	350	
ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga				1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg	355	360	365	
cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat				1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp	370	375	380	

aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val 385 390 395 400	1200
tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys 405 410 415	1248
gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln 420 425 430	1296
aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly 435 440 445	1344
cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr 450 455 460	1392
gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu 465 470 475 480	1440
tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp 485 490 495	1488
aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile 500 505 510	1536
act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser 515 520 525	1584
att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys 530 535 540	1632
gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala 545 550 555 560	1680
gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr 565 570 575	1728
aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile 580 585 590	1776
tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr 595 600 605	1824

ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag	1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys	
610 615 620	

aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc	1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile	
625 630 635 640	

tat ata gat aag ata gaa ttt atc cca gta caa ttg taa	1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu	
645 650	

<210> 54  
 <211> 652  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Recombinant delta endotoxin

<400> 54

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
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Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
20 25 30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
35 40 45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
50 55 60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65 70 75 80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
85 90 95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
100 105 110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
115 120 125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
130 135 140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145 150 155 160

Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
165 170 175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Gly Phe Glu Val
---

180					185					190					
Leu	Phe	Leu	Pro	Thr	Tyr	Ala	Gln	Ala	Ala	Asn	Thr	His	Leu	Leu	Leu
		195					200					205			
Leu	Lys	Asp	Ala	Gln	Val	Phe	Gly	Glu	Glu	Trp	Gly	Tyr	Ser	Ser	Glu
	210					215					220				
Asp	Val	Ala	Glu	Phe	Tyr	His	Arg	Gln	Leu	Lys	Leu	Thr	Gln	Gln	Tyr
225					230					235					240
Thr	Asp	His	Cys	Val	Asn	Trp	Tyr	Asn	Val	Gly	Leu	Asn	Gly	Leu	Arg
				245					250					255	
Gly	Ser	Thr	Tyr	Asp	Ala	Trp	Val	Lys	Phe	Asn	Arg	Phe	Arg	Arg	Glu
			260					265					270		
Met	Thr	Leu	Thr	Val	Leu	Asp	Leu	Ile	Val	Leu	Phe	Pro	Phe	Tyr	Asp
		275					280					285			
Ile	Arg	Leu	Tyr	Ser	Lys	Gly	Val	Lys	Thr	Glu	Leu	Thr	Arg	Asp	Ile
	290					295						300			
Phe	Thr	Asp	Pro	Ile	Phe	Ser	Leu	Asn	Thr	Leu	Gln	Glu	Tyr	Gly	Pro
305					310					315					320
Thr	Phe	Leu	Ser	Ile	Glu	Asn	Ser	Ile	Arg	Lys	Pro	His	Leu	Phe	Asp
				325					330					335	
Tyr	Leu	Gln	Gly	Ile	Glu	Phe	His	Thr	Arg	Leu	Gln	Pro	Gly	Tyr	Phe
		340						345					350		
Gly	Lys	Asp	Ser	Phe	Asn	Tyr	Trp	Ser	Gly	Asn	Tyr	Val	Glu	Thr	Arg
		355					360					365			
Pro	Ser	Ile	Gly	Ser	Ser	Lys	Thr	Ile	Thr	Ser	Pro	Phe	Tyr	Gly	Asp
	370					375					380				
Lys	Ser	Thr	Glu	Pro	Val	Gln	Lys	Leu	Ser	Phe	Asp	Gly	Gln	Lys	Val
385					390					395					400
Tyr	Arg	Thr	Ile	Ala	Asn	Thr	Asp	Val	Ala	Ala	Trp	Pro	Asn	Gly	Lys
				405					410					415	
Val	Tyr	Leu	Gly	Val	Thr	Lys	Val	Asp	Phe	Ser	Gln	Tyr	Asp	Asp	Gln
		420						425					430		
Lys	Asn	Glu	Thr	Ser	Thr	Gln	Thr	Tyr	Asp	Ser	Lys	Arg	Asn	Asn	Gly
		435					440					445			
His	Val	Ser	Ala	Gln	Asp	Ser	Ile	Asp	Gln	Leu	Pro	Pro	Glu	Thr	Thr
	450					455					460				
Asp	Glu	Pro	Leu	Glu	Lys	Ala	Tyr	Ser	His	Gln	Leu	Asn	Tyr	Ala	Glu
465					470					475					480
Cys	Phe	Leu	Met	Gln	Asp	Arg	Arg	Gly	Thr	Ile	Pro	Phe	Phe	Thr	Trp



485										490					495				
Thr	His	Arg	Ser	Val	Asp	Phe	Phe	Asn	Thr	Ile	Asp	Ala	Glu	Lys	Ile				
			500					505					510						
Thr	Gln	Leu	Pro	Val	Val	Lys	Ala	Tyr	Ala	Leu	Ser	Ser	Gly	Ala	Ser				
		515					520					525							
Ile	Ile	Glu	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Asn	Leu	Leu	Phe	Leu	Lys				
	530					535					540								
Glu	Ser	Ser	Asn	Ser	Ile	Ala	Lys	Phe	Lys	Val	Thr	Leu	Asn	Ser	Ala				
545					550					555					560				
Ala	Leu	Leu	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg	Tyr	Ala	Ser	Thr	Thr				
				565					570					575					
Asn	Leu	Arg	Leu	Phe	Val	Gln	Asn	Ser	Asn	Asn	Asp	Phe	Leu	Val	Ile				
			580					585					590						
Tyr	Ile	Asn	Lys	Thr	Met	Asn	Lys	Asp	Asp	Asp	Leu	Thr	Tyr	Gln	Thr				
		595					600					605							
Phe	Asp	Leu	Ala	Thr	Thr	Asn	Ser	Asn	Met	Gly	Phe	Ser	Gly	Asp	Lys				
	610					615					620								
Asn	Glu	Leu	Ile	Ile	Gly	Ala	Glu	Ser	Phe	Val	Ser	Asn	Glu	Lys	Ile				
625					630					635					640				
Tyr	Ile	Asp	Lys	Ile	Glu	Phe	Ile	Pro	Val	Gln	Leu								
				645					650										

<210> 55  
 <211> 1956  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Recombinant delta endotoxin

<220>  
 <221> CDS  
 <222> (1)..(1953)

<400> 55																				
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Met	Asn	Pro	Asn	Asn	Arg	Ser	Glu	His	Asp	Thr	Ile	Lys	Val	Thr	Pro					
1				5					10					15						
aac	agt	gaa	ttg	caa	act	aac	cat	aat	caa	tat	cct	tta	gct	gac	aat					96
Asn	Ser	Glu	Leu	Gln	Thr	Asn	His	Asn	Gln	Tyr	Pro	Leu	Ala	Asp	Asn					
			20					25					30							
cca	aat	tca	aca	cta	gaa	gaa	tta	aat	tat	aaa	gaa	ttt	tta	aga	atg					144
Pro	Asn	Ser	Thr	Leu	Glu	Glu	Leu	Asn	Tyr	Lys	Glu	Phe	Leu	Arg	Met					

35	40	45	
act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp 50 55 60			192
gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val 65 70 75 80			240
gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu 85 90 95			288
aac act ata tgg cca agt gaa gac cca tgg aag gct ttt atg gca caa Asn Thr Ile Trp Pro Ser Glu Asp Pro Trp Lys Ala Phe Met Ala Gln 100 105 110			336
gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt aaa Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser Lys 115 120 125			384
gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat gtt Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr Val 130 135 140			432
aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga aat cca Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Asn Pro 145 150 155 160			480
cac agc caa ggt cga ata agg gaa ctt ttt tct caa gca gaa agt cat His Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser His 165 170 175			528
ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg ctg Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val Leu 180 185 190			576
ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta tta Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu Leu 195 200 205			624
aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa gat Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu Asp 210 215 220			672
gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac act Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr Thr 225 230 235 240			720
gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga ggt Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg Gly 245 250 255			768
tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa atg Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu Met 260 265 270			816

act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat att	864
Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp Ile	
275 280 285	
cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att ttt	912
Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile Phe	
290 295 300	
acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca act	960
Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro Thr	
305 310 315 320	
ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat tat	1008
Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp Tyr	
325 330 335	
tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt ggg	1056
Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe Gly	
340 345 350	
aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga cct	1104
Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg Pro	
355 360 365	
agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat aaa	1152
Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp Lys	
370 375 380	
tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt tat	1200
Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val Tyr	
385 390 395 400	
cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag gta	1248
Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys Val	
405 410 415	
tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa aaa	1296
Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln Lys	
420 425 430	
aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc cat	1344
Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly His	
435 440 445	
gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca gat	1392
Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr Asp	
450 455 460	
gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa tgt	1440
Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu Cys	
465 470 475 480	
ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg aca	1488
Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp Thr	
485 490 495	

cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att act	1536
His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile Thr	
500 505 510	
caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc att	1584
Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser Ile	
515 520 525	
att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa gaa	1632
Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys Glu	
530 535 540	
tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca gcc	1680
Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala Ala	
545 550 555 560	
ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act aac	1728
Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr Asn	
565 570 575	
tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc tac	1776
Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile Tyr	
580 585 590	
att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca ttt	1824
Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr Phe	
595 600 605	
gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag aat	1872
Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys Asn	
610 615 620	
gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc tat	1920
Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile Tyr	
625 630 635 640	
ata gat aag ata gaa ttt atc cca gta caa ttg taa	1956
Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu	
645 650	

<210> 56

<211> 651

<212> PRT

<213> Artificial sequence

<220>

<223> Recombinant delta endotoxin

<400> 56

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro	
1 5 10 15	
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn	
20 25 30	

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met  
 35 40 45  
 Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp  
 50 55 60  
 Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val  
 65 70 75 80  
 Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu  
 85 90 95  
 Asn Thr Ile Trp Pro Ser Glu Asp Pro Trp Lys Ala Phe Met Ala Gln  
 100 105 110  
 Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser Lys  
 115 120 125  
 Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr Val  
 130 135 140  
 Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Asn Pro  
 145 150 155 160  
 His Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser His  
 165 170 175  
 Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val Leu  
 180 185 190  
 Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu Leu  
 195 200 205  
 Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu Asp  
 210 215 220  
 Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr Thr  
 225 230 235 240  
 Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg Gly  
 245 250 255  
 Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu Met  
 260 265 270  
 Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp Ile  
 275 280 285  
 Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile Phe  
 290 295 300  
 Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro Thr  
 305 310 315 320  
 Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp Tyr  
 325 330 335

Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe Gly  
 340 345 350  
 Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg Pro  
 355 360 365  
 Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp Lys  
 370 375 380  
 Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val Tyr  
 385 390 395 400  
 Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys Val  
 405 410 415  
 Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln Lys  
 420 425 430  
 Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly His  
 435 440 445  
 Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr Asp  
 450 455 460  
 Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu Cys  
 465 470 475 480  
 Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp Thr  
 485 490 495  
 His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile Thr  
 500 505 510  
 Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser Ile  
 515 520 525  
 Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys Glu  
 530 535 540  
 Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala Ala  
 545 550 555 560  
 Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr Asn  
 565 570 575  
 Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile Tyr  
 580 585 590  
 Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr Phe  
 595 600 605  
 Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys Asn  
 610 615 620  
 Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile Tyr  
 625 630 635 640

Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu  
645 650

<210> 57  
<211> 1956  
<212> DNA  
<213> Artificial sequence .  
  
<220>  
<223> Recombinant delta endotoxin

<220>  
<221> CDS  
<222> (1)..(1953)

<400> 57  
atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct 48  
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro  
1 5 10 15  
  
aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat 96  
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn  
20 25 30  
  
cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg 144  
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met  
35 40 45  
  
act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat 192  
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp  
50 55 60  
  
gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta 240  
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val  
65 70 75 80  
  
gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt 288  
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu  
85 90 95  
  
aac act ata tgg cca agt gaa gac cca tgg aag gct ttt atg gca caa 336  
Asn Thr Ile Trp Pro Ser Glu Asp Pro Trp Lys Ala Phe Met Ala Gln  
100 105 110  
  
gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt aaa 384  
Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser Lys  
115 120 125  
  
gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat gtt 432  
Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr Val  
130 135 140  
  
aat gcg tta aat tcc tgg aag aaa ttt cac cat tct cgt cgt tct aaa 480  
Asn Ala Leu Asn Ser Trp Lys Lys Phe His His Ser Arg Arg Ser Lys  
145 150 155 160

aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt cat	528
Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser His	
165 170 175	
ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg ctg	576
Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val Leu	
180 185 190	
ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta tta	624
Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu Leu	
195 200 205	
aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa gat	672
Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu Asp	
210 215 220	
gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac act	720
Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr Thr	
225 230 235 240	
gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga ggt	768
Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg Gly	
245 250 255	
tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa atg	816
Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu Met	
260 265 270	
act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat att	864
Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp Ile	
275 280 285	
cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att ttt	912
Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile Phe	
290 295 300	
acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca act	960
Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro Thr	
305 310 315 320	
ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat tat	1008
Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp Tyr	
325 330 335	
tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt ggg	1056
Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe Gly	
340 345 350	
aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga cct	1104
Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg Pro	
355 360 365	
agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat aaa	1152
Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp Lys	
370 375 380	



tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt tat	1200
Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val Tyr	
385 390 395 400	
cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag gta	1248
Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys Val	
405 410 415	
tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa aaa	1296
Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln Lys	
420 425 430	
aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc cat	1344
Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly His	
435 440 445	
gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca gat	1392
Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr Asp	
450 455 460	
gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa tgt	1440
Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu Cys	
465 470 475 480	
ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg aca	1488
Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp Thr	
485 490 495	
cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att act	1536
His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile Thr	
500 505 510	
caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc att	1584
Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser Ile	
515 520 525	
att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa gaa	1632
Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys Glu	
530 535 540	
tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca gcc	1680
Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala Ala	
545 550 555 560	
ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act aac	1728
Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr Asn	
565 570 575	
tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc tac	1776
Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile Tyr	
580 585 590	
att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca ttt	1824
Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr Phe	
595 600 605	
gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag aat	1872

Asp	Leu	Ala	Thr	Thr	Asn	Ser	Asn	Met	Gly	Phe	Ser	Gly	Asp	Lys	Asn	
610						615					620					
gaa	ctt	ata	ata	gga	gca	gaa	tct	ttc	gtt	tct	aat	gaa	aaa	atc	tat	1920
Glu	Leu	Ile	Ile	Gly	Ala	Glu	Ser	Phe	Val	Ser	Asn	Glu	Lys	Ile	Tyr	
625				630						635					640	
ata	gat	aag	ata	gaa	ttt	atc	cca	gta	caa	ttg	taa					1956
Ile	Asp	Lys	Ile	Glu	Phe	Ile	Pro	Val	Gln	Leu						
				645					650							

<210> 58  
 <211> 651  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Recombinant delta endotoxin

<400> 58

Met	Asn	Pro	Asn	Asn	Arg	Ser	Glu	His	Asp	Thr	Ile	Lys	Val	Thr	Pro	
1			5						10					15		
Asn	Ser	Glu	Leu	Gln	Thr	Asn	His	Asn	Gln	Tyr	Pro	Leu	Ala	Asp	Asn	
		20						25					30			
Pro	Asn	Ser	Thr	Leu	Glu	Glu	Leu	Asn	Tyr	Lys	Glu	Phe	Leu	Arg	Met	
		35					40					45				
Thr	Glu	Asp	Ser	Ser	Thr	Glu	Val	Leu	Asp	Asn	Ser	Thr	Val	Lys	Asp	
	50					55					60					
Ala	Val	Gly	Thr	Gly	Ile	Ser	Val	Val	Gly	Gln	Ile	Leu	Gly	Val	Val	
65				70						75					80	
Gly	Val	Pro	Phe	Ala	Gly	Ala	Leu	Thr	Ser	Phe	Tyr	Gln	Ser	Phe	Leu	
			85						90					95		
Asn	Thr	Ile	Trp	Pro	Ser	Glu	Asp	Pro	Trp	Lys	Ala	Phe	Met	Ala	Gln	
		100						105					110			
Val	Glu	Val	Leu	Ile	Asp	Lys	Lys	Ile	Glu	Glu	Tyr	Ala	Lys	Ser	Lys	
	115						120					125				
Ala	Leu	Ala	Glu	Leu	Gln	Gly	Leu	Gln	Asn	Asn	Phe	Glu	Asp	Tyr	Val	
	130					135					140					
Asn	Ala	Leu	Asn	Ser	Trp	Lys	Lys	Phe	His	His	Ser	Arg	Arg	Ser	Lys	
145				150						155					160	
Arg	Ser	Gln	Asp	Arg	Ile	Arg	Glu	Leu	Phe	Ser	Gln	Ala	Glu	Ser	His	
			165						170					175		
Phe	Arg	Asn	Ser	Met	Pro	Ser	Phe	Ala	Val	Ser	Lys	Phe	Glu	Val	Leu	
		180						185					190			

Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu Leu  
195 200 205  
Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu Asp  
210 215 220  
Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr Thr  
225 230 235 240  
Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg Gly  
245 250 255  
Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu Met  
260 265 270  
Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp Ile  
275 280 285  
Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile Phe  
290 295 300  
Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro Thr  
305 310 315 320  
Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp Tyr  
325 330 335  
Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe Gly  
340 345 350  
Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg Pro  
355 360 365  
Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp Lys  
370 375 380  
Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val Tyr  
385 390 395 400  
Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys Val  
405 410 415  
Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln Lys  
420 425 430  
Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly His  
435 440 445  
Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr Asp  
450 455 460  
Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu Cys  
465 470 475 480  
Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp Thr  
485 490 495

His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile Thr  
 500 505 510  
 Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser Ile  
 515 520 525  
 Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys Glu  
 530 535 540  
 Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala Ala  
 545 550 555 560  
 Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr Asn  
 565 570 575  
 Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile Tyr  
 580 585 590  
 Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr Phe  
 595 600 605  
 Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys Asn  
 610 615 620  
 Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile Tyr  
 625 630 635 640  
 Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu  
 645 650

<210> 59  
 <211> 1959  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Recombinant delta endotoxin

<220>  
 <221> CDS  
 <222> (1)..(1956)

<400> 59  
 atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct 48  
 Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro  
 1 5 10 15  
 aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat 96  
 Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn  
 20 25 30  
 cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg 144  
 Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met  
 35 40 45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp 50 55 60	192
gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val 65 70 75 80	240
gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu 85 90 95	288
aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala 100 105 110	336
caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser 115 120 125	384
aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr 130 135 140	432
gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser 145 150 155 160	480
aaa aga agc caa ggt cga ata agg gaa ctt ttt tct caa gca gaa agt Lys Arg Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser 165 170 175	528
cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val 180 185 190	576
ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu 195 200 205	624
tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu 210 215 220	672
gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr 225 230 235 240	720
act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg 245 250 255	768
ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu 260 265 270	816

atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat	864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp	
275 280 285	
att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att	912
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile	
290 295 300	
ttt acg gat cca att ttt acc ctt aat aca cta cag aag tac gga cca	960
Phe Thr Asp Pro Ile Phe Thr Leu Asn Thr Leu Gln Lys Tyr Gly Pro	
305 310 315 320	
act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat	1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp	
325 330 335	
tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt	1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe	
340 345 350	
ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga	1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg	
355 360 365	
cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat	1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp	
370 375 380	
aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt	1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val	
385 390 395 400	
tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag	1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys	
405 410 415	
gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa	1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln	
420 425 430	
aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc	1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly	
435 440 445	
cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca	1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr	
450 455 460	
gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa	1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu	
465 470 475 480	
tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg	1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp	
485 490 495	
aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att	1536

Thr	His	Arg	Ser	Val	Asp	Phe	Phe	Asn	Thr	Ile	Asp	Ala	Glu	Lys	Ile		
			500					505					510				
act	caa	ctt	cca	gta	gtg	aaa	gca	tat	gcc	ttg	tct	tca	ggt	gct	tcc	1584	
Thr	Gln	Leu	Pro	Val	Val	Lys	Ala	Tyr	Ala	Leu	Ser	Ser	Gly	Ala	Ser		
		515					520					525					
att	att	gaa	ggt	cca	gga	ttc	aca	gga	gga	aat	tta	cta	ttc	cta	aaa	1632	
Ile	Ile	Glu	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Asn	Leu	Leu	Phe	Leu	Lys		
		530				535					540						
gaa	tct	agt	aat	tca	att	gct	aaa	ttt	aaa	ggt	aca	tta	aat	tca	gca	1680	
Glu	Ser	Ser	Asn	Ser	Ile	Ala	Lys	Phe	Lys	Val	Thr	Leu	Asn	Ser	Ala		
545					550					555					560		
gcc	ttg	tta	caa	cga	tat	cgt	gta	aga	ata	cgc	tat	gct	tct	acc	act	1728	
Ala	Leu	Leu	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg	Tyr	Ala	Ser	Thr	Thr		
				565					570					575			
aac	tta	cga	ctt	ttt	gtg	caa	aat	tca	aac	aat	gat	ttt	ctt	gtc	atc	1776	
Asn	Leu	Arg	Leu	Phe	Val	Gln	Asn	Ser	Asn	Asn	Asp	Phe	Leu	Val	Ile		
			580					585					590				
tac	att	aat	aaa	act	atg	aat	aaa	gat	gat	gat	tta	aca	tat	caa	aca	1824	
Tyr	Ile	Asn	Lys	Thr	Met	Asn	Lys	Asp	Asp	Asp	Leu	Thr	Tyr	Gln	Thr		
		595					600					605					
ttt	gat	ctc	gca	act	act	aat	tct	aat	atg	ggg	ttc	tcg	ggt	gat	aag	1872	
Phe	Asp	Leu	Ala	Thr	Thr	Asn	Ser	Asn	Met	Gly	Phe	Ser	Gly	Asp	Lys		
	610					615					620						
aat	gaa	ctt	ata	ata	gga	gca	gaa	tct	ttc	ggt	tct	aat	gaa	aaa	atc	1920	
Asn	Glu	Leu	Ile	Ile	Gly	Ala	Glu	Ser	Phe	Val	Ser	Asn	Glu	Lys	Ile		
625					630					635					640		
tat	ata	gat	aag	ata	gaa	ttt	atc	cca	gta	caa	ttg	taa				1959	
Tyr	Ile	Asp	Lys	Ile	Glu	Phe	Ile	Pro	Val	Gln	Leu						
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<210> 60

<211> 652

<212> PRT

<213> Artificial sequence

<220>

<223> Recombinant delta endotoxin

<400> 60

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Asn	Ser	Glu	Leu	Gln	Thr	Asn	His	Asn	Gln	Tyr	Pro	Leu	Ala	Asp	Asn		
			20					25					30				
Pro	Asn	Ser	Thr	Leu	Glu	Glu	Leu	Asn	Tyr	Lys	Glu	Phe	Leu	Arg	Met		

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Thr	Glu	Asp	Ser	Ser	Thr	Glu	Val	Leu	Asp	Asn	Ser	Thr	Val	Lys	Asp
50					55					60					
Ala	Val	Gly	Thr	Gly	Ile	Ser	Val	Val	Gly	Gln	Ile	Leu	Gly	Val	Val
65					70					75					80
Gly	Val	Pro	Phe	Ala	Gly	Ala	Leu	Thr	Ser	Phe	Tyr	Gln	Ser	Phe	Leu
				85					90					95	
Asn	Thr	Ile	Trp	Pro	Ser	Asp	Ala	Asp	Pro	Trp	Lys	Ala	Phe	Met	Ala
			100					105					110		
Gln	Val	Glu	Val	Leu	Ile	Asp	Lys	Lys	Ile	Glu	Glu	Tyr	Ala	Lys	Ser
		115					120					125			
Lys	Ala	Leu	Ala	Glu	Leu	Gln	Gly	Leu	Gln	Asn	Asn	Phe	Glu	Asp	Tyr
130					135					140					
Val	Asn	Ala	Leu	Asn	Ser	Trp	Lys	Lys	Thr	Pro	Leu	Ser	Leu	Arg	Ser
145					150					155					160
Lys	Arg	Ser	Gln	Gly	Arg	Ile	Arg	Glu	Leu	Phe	Ser	Gln	Ala	Glu	Ser
				165					170					175	
His	Phe	Arg	Asn	Ser	Met	Pro	Ser	Phe	Ala	Val	Ser	Lys	Phe	Glu	Val
			180					185					190		
Leu	Phe	Leu	Pro	Thr	Tyr	Ala	Gln	Ala	Ala	Asn	Thr	His	Leu	Leu	Leu
		195					200					205			
Leu	Lys	Asp	Ala	Gln	Val	Phe	Gly	Glu	Glu	Trp	Gly	Tyr	Ser	Ser	Glu
210					215					220					
Asp	Val	Ala	Glu	Phe	Tyr	His	Arg	Gln	Leu	Lys	Leu	Thr	Gln	Gln	Tyr
225					230					235					240
Thr	Asp	His	Cys	Val	Asn	Trp	Tyr	Asn	Val	Gly	Leu	Asn	Gly	Leu	Arg
				245					250					255	
Gly	Ser	Thr	Tyr	Asp	Ala	Trp	Val	Lys	Phe	Asn	Arg	Phe	Arg	Arg	Glu
			260					265					270		
Met	Thr	Leu	Thr	Val	Leu	Asp	Leu	Ile	Val	Leu	Phe	Pro	Phe	Tyr	Asp
		275					280					285			
Ile	Arg	Leu	Tyr	Ser	Lys	Gly	Val	Lys	Thr	Glu	Leu	Thr	Arg	Asp	Ile
290					295					300					
Phe	Thr	Asp	Pro	Ile	Phe	Thr	Leu	Asn	Thr	Leu	Gln	Lys	Tyr	Gly	Pro
305					310					315					320
Thr	Phe	Leu	Ser	Ile	Glu	Asn	Ser	Ile	Arg	Lys	Pro	His	Leu	Phe	Asp
				325					330					335	
Tyr	Leu	Gln	Gly	Ile	Glu	Phe	His	Thr	Arg	Leu	Gln	Pro	Gly	Tyr	Phe



340	345	350
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg		
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Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp		
370	375	380
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val		
385	390	400
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys		
	405	410
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln		
	420	425
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly		
	435	440
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr		
	450	455
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu		
465	470	475
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp		
	485	490
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile		
	500	505
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser		
	515	520
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys		
	530	535
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala		
545	550	555
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr		
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Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile		
	580	585
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr		
	595	600
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys		
	610	615
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile		
625	630	635
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu		

<210> 61  
 <211> 1959  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Recombinant delta endotoxin

<220>  
 <221> CDS  
 <222> (1)..(1956)

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 aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat 96  
 Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn  
 20 25 30  
 cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg 144  
 Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met  
 35 40 45  
 act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat 192  
 Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp  
 50 55 60  
 gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta 240  
 Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val  
 65 70 75 80  
 gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt 288  
 Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu  
 85 90 95  
 aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca 336  
 Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala  
 100 105 110  
 caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt 384  
 Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser  
 115 120 125  
 aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat 432  
 Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr  
 130 135 140  
 gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt 480  
 Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser  
 145 150 155 160

aaa aga agc caa ggt cga ata agg gaa ctt ttt tct caa gca gaa agt Lys Arg Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser	528
165 170 175	
cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val	576
180 185 190	
ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu	624
195 200 205	
tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu	672
210 215 220	
gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr	720
225 230 235 240	
act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg	768
245 250 255	
ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu	816
260 265 270	
atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp	864
275 280 285	
gtt cgg tta tac cca aaa ggg gtt aaa aca gaa cta aca aga gac att Val Arg Leu Tyr Pro Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile	912
290 295 300	
tct acg gat cca att ttt gcc gtt aat act ctg tgg gaa tac gga cca Ser Thr Asp Pro Ile Phe Ala Val Asn Thr Leu Trp Glu Tyr Gly Pro	960
305 310 315 320	
act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp	1008
325 330 335	
tat tta cag ggg att gaa ttt cat acg cgt ctt cga cct ggt tac ttt Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Arg Pro Gly Tyr Phe	1056
340 345 350	
ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gca gaa act aga Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Ala Glu Thr Arg	1104
355 360 365	
cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp	1152
370 375 380	
aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt	1200

Lys	Ser	Thr	Glu	Pro	Val	Gln	Lys	Leu	Ser	Phe	Asp	Gly	Gln	Lys	Val		
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Tyr	Arg	Thr	Ile	Ala	Asn	Thr	Asp	Val	Ala	Ala	Trp	Pro	Asn	Gly	Lys		
				405				410						415			
gta	tat	tta	ggg	gtt	acg	aaa	gtt	gat	ttt	agt	caa	tat	gat	gat	caa	1296	
Val	Tyr	Leu	Gly	Val	Thr	Lys	Val	Asp	Phe	Ser	Gln	Tyr	Asp	Asp	Gln		
			420					425					430				
aaa	aat	gaa	act	agt	aca	caa	aca	tat	gat	tca	aaa	aga	aac	aat	ggc	1344	
Lys	Asn	Glu	Thr	Ser	Thr	Gln	Thr	Tyr	Asp	Ser	Lys	Arg	Asn	Asn	Gly		
		435					440					445					
cat	gta	agt	gca	cag	gat	tct	att	gac	caa	tta	ccg	cca	gaa	aca	aca	1392	
His	Val	Ser	Ala	Gln	Asp	Ser	Ile	Asp	Gln	Leu	Pro	Pro	Glu	Thr	Thr		
	450					455					460						
gat	gaa	cca	ctt	gaa	aaa	gca	tat	agt	cat	cag	ctt	aat	tac	gcg	gaa	1440	
Asp	Glu	Pro	Leu	Glu	Lys	Ala	Tyr	Ser	His	Gln	Leu	Asn	Tyr	Ala	Glu		
465					470					475					480		
tgt	ttc	tta	atg	cag	gac	cgt	cgt	gga	aca	att	cca	ttt	ttt	act	tgg	1488	
Cys	Phe	Leu	Met	Gln	Asp	Arg	Arg	Gly	Thr	Ile	Pro	Phe	Phe	Thr	Trp		
				485				490						495			
aca	cat	aga	agt	gta	gac	ttt	ttt	aat	aca	att	gat	gct	gaa	aag	att	1536	
Thr	His	Arg	Ser	Val	Asp	Phe	Phe	Asn	Thr	Ile	Asp	Ala	Glu	Lys	Ile		
			500					505					510				
act	caa	ctt	cca	gta	gtg	aaa	gca	tat	gcc	ttg	tct	tca	ggg	gct	tcc	1584	
Thr	Gln	Leu	Pro	Val	Val	Lys	Ala	Tyr	Ala	Leu	Ser	Ser	Gly	Ala	Ser		
		515					520				525						
att	att	gaa	ggg	cca	gga	ttc	aca	gga	gga	aat	tta	cta	ttc	cta	aaa	1632	
Ile	Ile	Glu	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Asn	Leu	Leu	Phe	Leu	Lys		
	530					535					540						
gaa	tct	agt	aat	tca	att	gct	aaa	ttt	aaa	gtt	aca	tta	aat	tca	gca	1680	
Glu	Ser	Ser	Asn	Ser	Ile	Ala	Lys	Phe	Lys	Val	Thr	Leu	Asn	Ser	Ala		
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Ala	Leu	Leu	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg	Tyr	Ala	Ser	Thr	Thr		
				565				570						575			
aac	tta	cga	ctt	ttt	gtg	caa	aat	tca	aac	aat	gat	ttt	ctt	gtc	atc	1776	
Asn	Leu	Arg	Leu	Phe	Val	Gln	Asn	Ser	Asn	Asn	Asp	Phe	Leu	Val	Ile		
			580					585					590				
tac	att	aat	aaa	act	atg	aat	aaa	gat	gat	gat	tta	aca	tat	caa	aca	1824	
Tyr	Ile	Asn	Lys	Thr	Met	Asn	Lys	Asp	Asp	Asp	Leu	Thr	Tyr	Gln	Thr		
		595					600					605					
ttt	gat	ctc	gca	act	act	aat	tct	aat	atg	ggg	ttc	tcg	ggg	gat	aag	1872	
Phe	Asp	Leu	Ala	Thr	Thr	Asn	Ser	Asn	Met	Gly	Phe	Ser	Gly	Asp	Lys		

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aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc			1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile			
625	630	635	640
tat ata gat aag ata gaa ttt atc cca gta caa ttg taa			1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu			
	645	650	

<210> 62  
 <211> 652  
 <212> PRT  
 <213> Artificial sequence  
  
 <220>  
 <223> Recombinant delta endotoxin  
  
 <400> 62

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Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met	
35 40 45	
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp	
50 55 60	
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val	
65 70 75 80	
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu	
85 90 95	
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala	
100 105 110	
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser	
115 120 125	
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr	
130 135 140	
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser	
145 150 155 160	
Lys Arg Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser	
165 170 175	
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val	
180 185 190	

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu  
 195 200 205  
 Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu  
 210 215 220  
 Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr  
 225 230 235 240  
 Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg  
 245 250 255  
 Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu  
 260 265 270  
 Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp  
 275 280 285  
 Val Arg Leu Tyr Pro Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile  
 290 295 300  
 Ser Thr Asp Pro Ile Phe Ala Val Asn Thr Leu Trp Glu Tyr Gly Pro  
 305 310 315 320  
 Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp  
 325 330 335  
 Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Arg Pro Gly Tyr Phe  
 340 345 350  
 Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Ala Glu Thr Arg  
 355 360 365  
 Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp  
 370 375 380  
 Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val  
 385 390 395 400  
 Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys  
 405 410 415  
 Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln  
 420 425 430  
 Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly  
 435 440 445  
 His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr  
 450 455 460  
 Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu  
 465 470 475 480  
 Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp  
 485 490 495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile  
 500 505 510  
 Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser  
 515 520 525  
 Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys  
 530 535 540  
 Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala  
 545 550 555 560  
 Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr  
 565 570 575  
 Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile  
 580 585 590  
 Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr  
 595 600 605  
 Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys  
 610 615 620  
 Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile  
 625 630 635 640  
 Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu  
 645 650

<210> 63  
 <211> 1959  
 <212> DNA  
 <213> Artificial sequence  
 <220>  
 <223> Recombinant delta endotoxin

<220>  
 <221> CDS  
 <222> (1)..(1956)

<400> 63  
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 Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro  
 1 5 10 15  
 aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat 96  
 Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn  
 20 25 30  
 cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg 144  
 Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met  
 35 40 45  
 act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat 192  
 Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp  
 50 55 60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val 65 70 75 80	240
gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu 85 90 95	288
aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala 100 105 110	336
caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser 115 120 125	384
aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr 130 135 140	432
gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser 145 150 155 160	480
aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser 165 170 175	528
cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val 180 185 190	576
ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu 195 200 205	624
tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu 210 215 220	672
gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr 225 230 235 240	720
act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg 245 250 255	768
ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu 260 265 270	816
atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp 275 280 285	864



gtt cgg tta tac cca aaa ggg gtt aaa aca gaa cta aca aga gac att	912
Val Arg Leu Tyr Pro Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile	
290 295 300	
ttt acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca	960
Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro	
305 310 315 320	
act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat	1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp	
325 330 335	
tat tta cag ggg att gaa ttt cat acg cgt ctt cga cct ggt tac ttt	1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Arg Pro Gly Tyr Phe	
340 345 350	
ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga	1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg	
355 360 365	
cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat	1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp	
370 375 380	
aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt	1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val	
385 390 395 400	
tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag	1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys	
405 410 415	
gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa	1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln	
420 425 430	
aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc	1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly	
435 440 445	
cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca	1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr	
450 455 460	
gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa	1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu	
465 470 475 480	
tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg	1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp	
485 490 495	
aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att	1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile	
500 505 510	
act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc	1584

Thr	Gln	Leu	Pro	Val	Val	Lys	Ala	Tyr	Ala	Leu	Ser	Ser	Gly	Ala	Ser		
		515					520					525					
att	att	gaa	ggt	cca	gga	ttc	aca	gga	gga	aat	tta	cta	ttc	cta	aaa	1632	
Ile	Ile	Glu	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Asn	Leu	Leu	Phe	Leu	Lys		
	530					535					540						
gaa	tct	agt	aat	tca	att	gct	aaa	ttt	aaa	gtt	aca	tta	aat	tca	gca	1680	
Glu	Ser	Ser	Asn	Ser	Ile	Ala	Lys	Phe	Lys	Val	Thr	Leu	Asn	Ser	Ala		
545					550					555					560		
gcc	ttg	tta	caa	cga	tat	cgt	gta	aga	ata	cgc	tat	gct	tct	acc	act	1728	
Ala	Leu	Leu	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg	Tyr	Ala	Ser	Thr	Thr		
				565					570					575			
aac	tta	cga	ctt	ttt	gtg	caa	aat	tca	aac	aat	gat	ttt	ctt	gtc	atc	1776	
Asn	Leu	Arg	Leu	Phe	Val	Gln	Asn	Ser	Asn	Asn	Asp	Phe	Leu	Val	Ile		
			580					585					590				
tac	att	aat	aaa	act	atg	aat	aaa	gat	gat	gat	tta	aca	tat	caa	aca	1824	
Tyr	Ile	Asn	Lys	Thr	Met	Asn	Lys	Asp	Asp	Asp	Leu	Thr	Tyr	Gln	Thr		
		595					600					605					
ttt	gat	ctc	gca	act	act	aat	tct	aat	atg	ggg	ttc	tcg	ggt	gat	aag	1872	
Phe	Asp	Leu	Ala	Thr	Thr	Asn	Ser	Asn	Met	Gly	Phe	Ser	Gly	Asp	Lys		
	610					615					620						
aat	gaa	ctt	ata	ata	gga	gca	gaa	tct	ttc	gtt	tct	aat	gaa	aaa	atc	1920	
Asn	Glu	Leu	Ile	Ile	Gly	Ala	Glu	Ser	Phe	Val	Ser	Asn	Glu	Lys	Ile		
625					630					635					640		
tat	ata	gat	aag	ata	gaa	ttt	atc	cca	gta	caa	ttg	taa				1959	
Tyr	Ile	Asp	Lys	Ile	Glu	Phe	Ile	Pro	Val	Gln	Leu						
				645					650								

<210> 64

<211> 652

<212> PRT

<213> Artificial sequence

<220>

<223> Recombinant delta endotoxin

<400> 64

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Asn	Ser	Glu	Leu	Gln	Thr	Asn	His	Asn	Gln	Tyr	Pro	Leu	Ala	Asp	Asn		
		20						25					30				

Pro	Asn	Ser	Thr	Leu	Glu	Glu	Leu	Asn	Tyr	Lys	Glu	Phe	Leu	Arg	Met		
		35					40					45					

Thr	Glu	Asp	Ser	Ser	Thr	Glu	Val	Leu	Asp	Asn	Ser	Thr	Val	Lys	Asp		
	50					55					60						

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val  
 65 70 75 80  
 Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu  
 85 90 95  
 Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala  
 100 105 110  
 Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser  
 115 120 125  
 Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr  
 130 135 140  
 Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser  
 145 150 155 160  
 Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser  
 165 170 175  
 His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val  
 180 185 190  
 Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu  
 195 200 205  
 Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu  
 210 215 220  
 Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr  
 225 230 235 240  
 Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg  
 245 250 255  
 Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu  
 260 265 270  
 Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp  
 275 280 285  
 Val Arg Leu Tyr Pro Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile  
 290 295 300  
 Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro  
 305 310 315 320  
 Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp  
 325 330 335  
 Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Arg Pro Gly Tyr Phe  
 340 345 350  
 Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg  
 355 360 365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp  
 370 375 380  
 Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val  
 385 390 395 400  
 Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys  
 405 410 415  
 Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln  
 420 425 430  
 Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly  
 435 440 445  
 His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr  
 450 455 460  
 Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu  
 465 470 475 480  
 Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp  
 485 490 495  
 Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile  
 500 505 510  
 Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser  
 515 520 525  
 Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys  
 530 535 540  
 Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala  
 545 550 555 560  
 Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr  
 565 570 575  
 Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile  
 580 585 590  
 Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr  
 595 600 605  
 Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys  
 610 615 620  
 Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile  
 625 630 635 640  
 Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu  
 645 650

<210> 65  
 <211> 1959

<212> DNA  
 <213> Artificial sequence

<220>  
 <223> Recombinant delta endotoxin

<220>  
 <221> CDS  
 <222> (1)..(1956)

<400> 65  
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 1 5 10 15

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat 96  
 Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn  
 20 25 30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg 144  
 Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met  
 35 40 45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat 192  
 Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp  
 50 55 60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta 240  
 Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val  
 65 70 75 80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt 288  
 Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu  
 85 90 95

aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca 336  
 Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala  
 100 105 110

caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt 384  
 Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser  
 115 120 125

aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat 432  
 Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr  
 130 135 140

gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt 480  
 Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser  
 145 150 155 160

aaa aga agc caa ggt cga ata agg gaa ctt ttt tct caa gca gaa agt 528  
 Lys Arg Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser  
 165 170 175

cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg 576

His	Phe	Arg	Asn	Ser	Met	Pro	Ser	Phe	Ala	Val	Ser	Lys	Phe	Glu	Val		
			180					185					190				
ctg	ttt	cta	cca	aca	tat	gca	caa	gct	gca	aat	aca	cat	tta	ttg	cta		624
Leu	Phe	Leu	Pro	Thr	Tyr	Ala	Gln	Ala	Ala	Asn	Thr	His	Leu	Leu	Leu		
		195					200					205					
tta	aaa	gat	gct	caa	gtt	ttt	gga	gaa	gaa	tgg	gga	tat	tct	tca	gaa		672
Leu	Lys	Asp	Ala	Gln	Val	Phe	Gly	Glu	Glu	Trp	Gly	Tyr	Ser	Ser	Glu		
	210					215					220						
gat	gtt	gct	gaa	ttt	tat	cat	aga	caa	tta	aaa	ctt	aca	caa	caa	tac		720
Asp	Val	Ala	Glu	Phe	Tyr	His	Arg	Gln	Leu	Lys	Leu	Thr	Gln	Gln	Tyr		
225					230					235					240		
act	gac	cat	tgt	gtt	aat	tgg	tat	aat	gtt	gga	tta	aat	ggt	tta	aga		768
Thr	Asp	His	Cys	Val	Asn	Trp	Tyr	Asn	Val	Gly	Leu	Asn	Gly	Leu	Arg		
				245					250					255			
ggt	tca	act	tat	gat	gca	tgg	gtc	aaa	ttt	aac	cgt	ttt	cgc	aga	gaa		816
Gly	Ser	Thr	Tyr	Asp	Ala	Trp	Val	Lys	Phe	Asn	Arg	Phe	Arg	Arg	Glu		
			260					265					270				
atg	act	tta	act	gta	tta	gat	cta	att	gta	ctt	ttc	cca	ttt	tat	gat		864
Met	Thr	Leu	Thr	Val	Leu	Asp	Leu	Ile	Val	Leu	Phe	Pro	Phe	Tyr	Asp		
		275					280					285					
att	cgg	tta	tac	tca	aaa	ggg	gtt	aaa	aca	gaa	cta	aca	aga	gac	att		912
Ile	Arg	Leu	Tyr	Ser	Lys	Gly	Val	Lys	Thr	Glu	Leu	Thr	Arg	Asp	Ile		
	290					295					300						
ttt	acg	gat	cca	att	ttt	tta	ctt	aat	act	ctt	cag	gag	tat	gga	cca		960
Phe	Thr	Asp	Pro	Ile	Phe	Leu	Leu	Asn	Thr	Leu	Gln	Glu	Tyr	Gly	Pro		
305				310						315					320		
act	ttt	ttg	agt	ata	gaa	aac	tct	att	cga	aaa	cct	cat	tta	ttt	gat		1008
Thr	Phe	Leu	Ser	Ile	Glu	Asn	Ser	Ile	Arg	Lys	Pro	His	Leu	Phe	Asp		
				325					330					335			
tat	tta	cag	ggg	att	gaa	ttt	cat	acg	cgt	ctt	caa	cct	ggt	tac	ttt		1056
Tyr	Leu	Gln	Gly	Ile	Glu	Phe	His	Thr	Arg	Leu	Gln	Pro	Gly	Tyr	Phe		
			340					345					350				
ggg	aaa	gat	tct	ttc	aat	tat	tgg	tct	ggt	aat	tat	gta	gaa	act	aga		1104
Gly	Lys	Asp	Ser	Phe	Asn	Tyr	Trp	Ser	Gly	Asn	Tyr	Val	Glu	Thr	Arg		
		355					360					365					
cct	agt	ata	gga	tct	agt	aag	aca	att	act	tcc	cca	ttt	tat	gga	gat		1152
Pro	Ser	Ile	Gly	Ser	Ser	Lys	Thr	Ile	Thr	Ser	Pro	Phe	Tyr	Gly	Asp		
		370				375					380						
aaa	tct	act	gaa	cct	gta	caa	aag	cta	agc	ttt	gat	gga	caa	aaa	gtt		1200
Lys	Ser	Thr	Glu	Pro	Val	Gln	Lys	Leu	Ser	Phe	Asp	Gly	Gln	Lys	Val		
385					390					395					400		
tat	cga	act	ata	gct	aat	aca	gac	gta	gcg	gct	tgg	ccg	aat	ggt	aag		1248
Tyr	Arg	Thr	Ile	Ala	Asn	Thr	Asp	Val	Ala	Ala	Trp	Pro	Asn	Gly	Lys		

405										410					415					
gta	tat	tta	ggt	ggt	acg	aaa	ggt	gat	ttt	agt	caa	tat	gat	gat	caa	1296				
Val	Tyr	Leu	Gly	Val	Thr	Lys	Val	Asp	Phe	Ser	Gln	Tyr	Asp	Asp	Gln					
		420						425					430							
aaa	aat	gaa	act	agt	aca	caa	aca	tat	gat	tca	aaa	aga	aac	aat	ggc	1344				
Lys	Asn	Glu	Thr	Ser	Thr	Gln	Thr	Tyr	Asp	Ser	Lys	Arg	Asn	Asn	Gly					
		435					440					445								
cat	gta	agt	gca	cag	gat	tct	att	gac	caa	tta	ccg	cca	gaa	aca	aca	1392				
His	Val	Ser	Ala	Gln	Asp	Ser	Ile	Asp	Gln	Leu	Pro	Pro	Glu	Thr	Thr					
	450					455					460									
gat	gaa	cca	ctt	gaa	aaa	gca	tat	agt	cat	cag	ctt	aat	tac	gcg	gaa	1440				
Asp	Glu	Pro	Leu	Glu	Lys	Ala	Tyr	Ser	His	Gln	Leu	Asn	Tyr	Ala	Glu					
465					470					475					480					
tgt	ttc	tta	atg	cag	gac	cgt	cgt	gga	aca	att	cca	ttt	ttt	act	tgg	1488				
Cys	Phe	Leu	Met	Gln	Asp	Arg	Arg	Gly	Thr	Ile	Pro	Phe	Phe	Thr	Trp					
				485					490					495						
aca	cat	aga	agt	gta	gac	ttt	ttt	aat	aca	att	gat	gct	gaa	aag	att	1536				
Thr	His	Arg	Ser	Val	Asp	Phe	Phe	Asn	Thr	Ile	Asp	Ala	Glu	Lys	Ile					
		500						505					510							
act	caa	ctt	cca	gta	gtg	aaa	gca	tat	gcc	ttg	tct	tca	ggt	gct	tcc	1584				
Thr	Gln	Leu	Pro	Val	Val	Lys	Ala	Tyr	Ala	Leu	Ser	Ser	Gly	Ala	Ser					
		515					520					525								
att	att	gaa	ggt	cca	gga	ttc	aca	gga	gga	aat	tta	cta	ttc	cta	aaa	1632				
Ile	Ile	Glu	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Asn	Leu	Leu	Phe	Leu	Lys					
	530					535					540									
gaa	tct	agt	aat	tca	att	gct	aaa	ttt	aaa	ggt	aca	tta	aat	tca	gca	1680				
Glu	Ser	Ser	Asn	Ser	Ile	Ala	Lys	Phe	Lys	Val	Thr	Leu	Asn	Ser	Ala					
545					550					555					560					
gcc	ttg	tta	caa	cga	tat	cgt	gta	aga	ata	cgc	tat	gct	tct	acc	act	1728				
Ala	Leu	Leu	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg	Tyr	Ala	Ser	Thr	Thr					
				565				570						575						
aac	tta	cga	ctt	ttt	gtg	caa	aat	tca	aac	aat	gat	ttt	ctt	gtc	atc	1776				
Asn	Leu	Arg	Leu	Phe	Val	Gln	Asn	Ser	Asn	Asn	Asp	Phe	Leu	Val	Ile					
			580					585					590							
tac	att	aat	aaa	act	atg	aat	aaa	gat	gat	gat	tta	aca	tat	caa	aca	1824				
Tyr	Ile	Asn	Lys	Thr	Met	Asn	Lys	Asp	Asp	Asp	Leu	Thr	Tyr	Gln	Thr					
		595					600					605								
ttt	gat	ctc	gca	act	act	aat	tct	aat	atg	ggg	ttc	tcg	ggt	gat	aag	1872				
Phe	Asp	Leu	Ala	Thr	Thr	Asn	Ser	Asn	Met	Gly	Phe	Ser	Gly	Asp	Lys					
	610					615					620									
aat	gaa	ctt	ata	ata	gga	gca	gaa	tct	ttc	gtt	tct	aat	gaa	aaa	atc	1920				
Asn	Glu	Leu	Ile	Ile	Gly	Ala	Glu	Ser	Phe	Val	Ser	Asn	Glu	Lys	Ile					
625					630					635					640					

tat ata gat aag ata gaa ttt atc cca gta caa ttg taa  
 Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu  
 645 650

1959

<210> 66  
 <211> 652  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Recombinant delta endotoxin

<400> 66

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro  
 1 5 10 15  
 Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn  
 20 25 30  
 Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met  
 35 40 45  
 Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp  
 50 55 60  
 Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val  
 65 70 75 80  
 Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu  
 85 90 95  
 Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala  
 100 105 110  
 Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser  
 115 120 125  
 Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr  
 130 135 140  
 Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser  
 145 150 155 160  
 Lys Arg Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser  
 165 170 175  
 His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val  
 180 185 190  
 Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu  
 195 200 205  
 Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu  
 210 215 220



Asp	Val	Ala	Glu	Phe	Tyr	His	Arg	Gln	Leu	Lys	Leu	Thr	Gln	Gln	Tyr	225	230	235	240
Thr	Asp	His	Cys	Val	Asn	Trp	Tyr	Asn	Val	Gly	Leu	Asn	Gly	Leu	Arg	245	250	255	
Gly	Ser	Thr	Tyr	Asp	Ala	Trp	Val	Lys	Phe	Asn	Arg	Phe	Arg	Arg	Glu	260	265	270	
Met	Thr	Leu	Thr	Val	Leu	Asp	Leu	Ile	Val	Leu	Phe	Pro	Phe	Tyr	Asp	275	280	285	
Ile	Arg	Leu	Tyr	Ser	Lys	Gly	Val	Lys	Thr	Glu	Leu	Thr	Arg	Asp	Ile	290	295	300	
Phe	Thr	Asp	Pro	Ile	Phe	Leu	Leu	Asn	Thr	Leu	Gln	Glu	Tyr	Gly	Pro	305	310	315	320
Thr	Phe	Leu	Ser	Ile	Glu	Asn	Ser	Ile	Arg	Lys	Pro	His	Leu	Phe	Asp	325	330	335	
Tyr	Leu	Gln	Gly	Ile	Glu	Phe	His	Thr	Arg	Leu	Gln	Pro	Gly	Tyr	Phe	340	345	350	
Gly	Lys	Asp	Ser	Phe	Asn	Tyr	Trp	Ser	Gly	Asn	Tyr	Val	Glu	Thr	Arg	355	360	365	
Pro	Ser	Ile	Gly	Ser	Ser	Lys	Thr	Ile	Thr	Ser	Pro	Phe	Tyr	Gly	Asp	370	375	380	
Lys	Ser	Thr	Glu	Pro	Val	Gln	Lys	Leu	Ser	Phe	Asp	Gly	Gln	Lys	Val	385	390	395	400
Tyr	Arg	Thr	Ile	Ala	Asn	Thr	Asp	Val	Ala	Ala	Trp	Pro	Asn	Gly	Lys	405	410	415	
Val	Tyr	Leu	Gly	Val	Thr	Lys	Val	Asp	Phe	Ser	Gln	Tyr	Asp	Asp	Gln	420	425	430	
Lys	Asn	Glu	Thr	Ser	Thr	Gln	Thr	Tyr	Asp	Ser	Lys	Arg	Asn	Asn	Gly	435	440	445	
His	Val	Ser	Ala	Gln	Asp	Ser	Ile	Asp	Gln	Leu	Pro	Pro	Glu	Thr	Thr	450	455	460	
Asp	Glu	Pro	Leu	Glu	Lys	Ala	Tyr	Ser	His	Gln	Leu	Asn	Tyr	Ala	Glu	465	470	475	480
Cys	Phe	Leu	Met	Gln	Asp	Arg	Arg	Gly	Thr	Ile	Pro	Phe	Phe	Thr	Trp	485	490	495	
Thr	His	Arg	Ser	Val	Asp	Phe	Phe	Asn	Thr	Ile	Asp	Ala	Glu	Lys	Ile	500	505	510	
Thr	Gln	Leu	Pro	Val	Val	Lys	Ala	Tyr	Ala	Leu	Ser	Ser	Gly	Ala	Ser	515	520	525	

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys  
 530 535 540  
 Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala  
 545 550 555 560  
 Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr  
 565 570 575  
 Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile  
 580 585 590  
 Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr  
 595 600 605  
 Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys  
 610 615 620  
 Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile  
 625 630 635 640  
 Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu  
 645 650

<210> 67  
 <211> 1959  
 <212> DNA  
 <213> Artificial sequence  
 <220>  
 <223> Recombinant delta endotoxin

<220>  
 <221> CDS  
 <222> (1)..(1956)

<400> 67  
 atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct 48  
 Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro  
 1 5 10 15  
 aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat 96  
 Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn  
 20 25 30  
 cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg 144  
 Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met  
 35 40 45  
 act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat 192  
 Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp  
 50 55 60  
 gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta 240  
 Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val

65	70	75	80	
gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt				288
Gly Val Pro Phe	Ala Gly Ala Leu Thr	Ser Phe Tyr Gln Ser	Phe Leu	
	85	90	95	
aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca				336
Asn Thr Ile Trp	Pro Ser Asp Ala Asp	Pro Trp Lys Ala Phe	Met Ala	
	100	105	110	
caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt				384
Gln Val Glu Val Leu Ile Asp	Lys Lys Ile Glu Glu Tyr	Ala Lys Ser		
	115	120	125	
aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat				432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr				
	130	135	140	
gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt				480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser				
	145	150	155	160
aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt				528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser				
	165	170	175	
cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg				576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val				
	180	185	190	
ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta				624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu				
	195	200	205	
tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa				672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu				
	210	215	220	
gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac				720
Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr				
	225	230	235	240
act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga				768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg				
	245	250	255	
ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa				816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu				
	260	265	270	
atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat				864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp				
	275	280	285	
att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att				912
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile				
	290	295	300	

ttt acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca	960
Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro	
305 310 315 320	
act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat	1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp	
325 330 335	
tat tta cag ggg att gaa ttt cat acg cgt ctt cga cct ggt tac ttt	1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Arg Pro Gly Tyr Phe	
340 345 350	
ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga	1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg	
355 360 365	
cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat	1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp	
370 375 380	
aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt	1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val	
385 390 395 400	
tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag	1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys	
405 410 415	
gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa	1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln	
420 425 430	
aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc	1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly	
435 440 445	
cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca	1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr	
450 455 460	
gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa	1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu	
465 470 475 480	
tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg	1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp	
485 490 495	
aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att	1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile	
500 505 510	
act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc	1584
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser	
515 520 525	

att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa	1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys	
530 535 540	
gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca	1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala	
545 550 555 560	
gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act	1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr	
565 570 575	
aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc	1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile	
580 585 590	
tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca	1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr	
595 600 605	
ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag	1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys	
610 615 620	
aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc	1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile	
625 630 635 640	
tat ata gat aag ata gaa ttt atc cca gta caa ttg taa	1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu	
645 650	

<210> 68  
 <211> 652  
 <212> PRT  
 <213> Artificial sequence  
  
 <220>  
 <223> Recombinant delta endotoxin  
  
 <400> 68

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro	
1 5 10 15	
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn	
20 25 30	
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met	
35 40 45	
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp	
50 55 60	
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val	
65 70 75 80	

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu  
 85 90 95  
 Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala  
 100 105 110  
 Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser  
 115 120 125  
 Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr  
 130 135 140  
 Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser  
 145 150 155 160  
 Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser  
 165 170 175  
 His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val  
 180 185 190  
 Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu  
 195 200 205  
 Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu  
 210 215 220  
 Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr  
 225 230 235 240  
 Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg  
 245 250 255  
 Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu  
 260 265 270  
 Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp  
 275 280 285  
 Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile  
 290 295 300  
 Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro  
 305 310 315 320  
 Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp  
 325 330 335  
 Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Arg Pro Gly Tyr Phe  
 340 345 350  
 Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg  
 355 360 365  
 Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp  
 370 375 380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val  
 385 390 395 400  
 Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys  
 405 410 415  
 Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln  
 420 425 430  
 Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly  
 435 440 445  
 His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr  
 450 455 460  
 Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu  
 465 470 475 480  
 Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp  
 485 490 495  
 Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile  
 500 505 510  
 Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser  
 515 520 525  
 Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys  
 530 535 540  
 Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala  
 545 550 555 560  
 Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr  
 565 570 575  
 Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile  
 580 585 590  
 Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr  
 595 600 605  
 Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys  
 610 615 620  
 Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile  
 625 630 635 640  
 Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu  
 645 650

<210> 69  
 <211> 1482  
 <212> DNA  
 <213> Artificial sequence  
 <220>

<223> Recombinant delta endotoxin

<220>

<221> CDS

<222> (1)..(1479)

<400> 69

agt aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa	48
Ser Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu	
1 5 10 15	
agt cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa	96
Ser His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu	
20 25 30	
gtg ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg	144
Val Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu	
35 40 45	
cta tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca	192
Leu Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser	
50 55 60	
gaa gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa	240
Glu Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln	
65 70 75 80	
tac act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta	288
Tyr Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu	
85 90 95	
aga ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga	336
Arg Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg	
100 105 110	
gaa atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat	384
Glu Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr	
115 120 125	
gat att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac	432
Asp Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp	
130 135 140	
att ttt acg gat cca att ttt tca ctt aat act ctt cag gag tat gga	480
Ile Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly	
145 150 155 160	
cca act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt	528
Pro Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe	
165 170 175	
gat tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac	576
Asp Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr	
180 185 190	
ttt ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act	624
Phe Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr	



195	200	205	
aga cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga Arg Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly 210 215 220			672
gat aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa Asp Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys 225 230 235 240			720
gtt tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt Val Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly 245 250 255			768
aag gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat Lys Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp 260 265 270			816
caa aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat Gln Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn 275 280 285			864
ggc cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca Gly His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr 290 295 300			912
aca gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg Thr Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala 305 310 315 320			960
gaa tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act Glu Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr 325 330 335			1008
tgg aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag Trp Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys 340 345 350			1056
att act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct Ile Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala 355 360 365			1104
tcc att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta Ser Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu 370 375 380			1152
aaa gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca Lys Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser 385 390 395 400			1200
gca gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc Ala Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr 405 410 415			1248
act aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc Thr Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val 420 425 430			1296

atc tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa	1344
Ile Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln	
435 440 445	
aca ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat	1392
Thr Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp	
450 455 460	
aag aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa	1440
Lys Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys	
465 470 475 480	
atc tat ata gat aag ata gaa ttt atc cca gta caa ttg taa	1482
Ile Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu	
485 490	

<210> 70  
 <211> 493  
 <212> PRT  
 <213> Artificial sequence  
  
 <220>  
 <223> Recombinant delta endotoxin  
  
 <400> 70

Ser Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu	
1 5 10 15	
Ser His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu	
20 25 30	
Val Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu	
35 40 45	
Leu Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser	
50 55 60	
Glu Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln	
65 70 75 80	
Tyr Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu	
85 90 95	
Arg Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg	
100 105 110	
Glu Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr	
115 120 125	
Asp Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp	
130 135 140	
Ile Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly	
145 150 155 160	

Pro Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe  
 165 170 175  
 Asp Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr  
 180 185 190  
 Phe Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr  
 195 200 205  
 Arg Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly  
 210 215 220  
 Asp Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys  
 225 230 235 240  
 Val Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly  
 245 250 255  
 Lys Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp  
 260 265 270  
 Gln Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn  
 275 280 285  
 Gly His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr  
 290 295 300  
 Thr Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala  
 305 310 315 320  
 Glu Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr  
 325 330 335  
 Trp Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys  
 340 345 350  
 Ile Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala  
 355 360 365  
 Ser Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu  
 370 375 380  
 Lys Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser  
 385 390 395 400  
 Ala Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr  
 405 410 415  
 Thr Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val  
 420 425 430  
 Ile Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln  
 435 440 445  
 Thr Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp  
 450 455 460

Lys Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys  
 465 470 475 480

Ile Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu  
 485 490

<210> 71  
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 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Synthetic Oligonucleotide

<400> 71  
 agacaactct acagtaaaag atg 23

<210> 72  
 <211> 20  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Synthetic Oligonucleotide

<400> 72  
 ggtaattggt caatagaatc 20

<210> 73  
 <211> 39  
 <212> DNA  
 <213> Artificial sequence

<220>  
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<220>  
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 <223> N = A, T, G, C (25% each)

<400> 73  
 cagaagatgt tgctgaattc nnncatagac aattaaaac 39

<210> 74  
 <211> 34  
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<220>  
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<220>  
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 <222> (19)..(21)  
 <223> N = A, T, G, C (25% each)  
  
 <400> 74  
 gatgttgctg aattctatnn nagacaatta aaac

34

<210> 75  
 <211> 33  
 <212> DNA  
 <213> Artificial sequence

<220>  
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<220>  
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 <222> (17)..(17)  
 <223> N = A, T, C (16% each); G (52%)

<220>  
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 <222> (18)..(18)  
 <223> N = T, G, C (10% each); A (70%)

<220>  
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 <223> N = A, T, G, C (25% each)

<400> 75  
 cccattttat gatattnnnt tataactcaaa agg

33

<210> 76  
 <211> 64  
 <212> DNA  
 <213> Artificial sequence

<220>  
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<220>  
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 <223> N = T, G, C (6% each); A (82%)

<220>  
 <221> misc\_feature  
 <222> (25)..(25)  
 <223> N = A, T, G (6% each); C (82%)

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<220>
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<222> (26)..(26)
<223> N = A, T, G, C (25% each)

<220>
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<222> (27)..(28)
<223> N = A, T, G (6% each); C (82%)

<220>
<221> misc_feature
<222> (29)..(29)
<223> N = A, T, G, C (25% each)

<220>
<221> misc_feature
<222> (30)..(30)
<223> N = A, T, G (6% each); C (82%)

<220>
<221> misc_feature
<222> (31)..(31)
<223> N = A, G, C (6% each); T (82%)

<220>
<221> misc_feature
<222> (32)..(32)
<223> N = A, T, G, C (25%)

<220>
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<222> (33)..(33)
<223> N = A, G, C (6% each); T (82%)

<220>
<221> misc_feature
<222> (34)..(34)
<223> N = A, T, G (6% each) ; C (82%)

<220>
<221> misc_feature
<222> (35)..(35)
<223> N = A, G, C (6% each); T (82%)

<220>
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<222> (36)..(36)
<223> N = A, T, G (6% each) ; C (82%)

<220>
<221> misc_feature
<222> (37)..(37)
<223> N = A, G, C (6% each); T (82%)

<220>

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<223> N = A, T, G, C (25% each)

<220>
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<222> (39)..(39)
<223> N = A, T, G (6% each); C (82%)

<220>
<221> misc_feature
<222> (40)..(40)
<223> N = A, T, C (6% each); G (82%)

<220>
<221> misc_feature
<222> (41)..(41)
<223> N = A, T, G, C (25% each)

<220>
<221> misc_feature
<222> (42)..(42)
<223> N = A, G, C (6% each); T (82%)

<220>
<221> misc_feature
<222> (43)..(43)
<223> N = A, T, G (6% each); C (82%)

<220>
<221> misc_feature
<222> (44)..(44)
<223> N = A, G, C (6% each); T (82%)

<400> 76
agctatgctg gtctcggaag aaannnnnnnn nnnnnnnnnnn nnnnaaaaga agccaagatc      60
gaat                                                                    64

<210> 77
<211> 40
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Oligonucleotide

<400> 77
ggtcacctag gtctctcttc caggaattta acgcattaac      40

<210> 78
<211> 65
<212> DNA
<213> Artificial sequence

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<220>  
 <223> Synthetic Oligonucleotide

<220>  
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 <222> (22)..(22)  
 <223> N = A, G, C (6% each); T (82%)

<220>  
 <221> misc\_feature  
 <222> (23)..(23)  
 <223> N = T, G, C (6% each); A (82%)

<220>  
 <221> misc\_feature  
 <222> (24)..(24)  
 <223> N = A, T, G (1% each); C (97%)

<220>  
 <221> misc\_feature  
 <222> (25)..(25)  
 <223> N = A, T, C (6% each); G (82%)

<220>  
 <221> misc\_feature  
 <222> (26)..(26)  
 <223> N = T, G, C (6% each); A (82%)

<220>  
 <221> misc\_feature  
 <222> (27)..(27)  
 <223> N = A, G, C (6% each); T (82%)

<220>  
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 <222> (28)..(28)  
 <223> N = T, G, C (6% each); A (82%)

<220>  
 <221> misc\_feature  
 <222> (29)..(29)  
 <223> N = A, G, C (6% each); T (82%)

<220>  
 <221> misc\_feature  
 <222> (30)..(30)  
 <223> N = A, G, C (6% each); T (82%)

<220>  
 <221> misc\_feature  
 <222> (31)..(31)  
 <223> N = T, G, C (6% each); A (82%)

<220>  
 <221> misc\_feature  
 <222> (32)..(33)



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<223> N = A, T, C (6% each); G (82%)

<220>
<221> misc_feature
<222> (34)..(34)
<223> N = A, T, G (15% each); C (55%)

<220>
<221> misc_feature
<222> (35)..(36)
<223> N = A, G, C (15% each); T (55%)

<220>
<221> misc_feature
<222> (37)..(37)
<223> N = A, G, C (6% each); T (82%)

<220>
<221> misc_feature
<222> (38)..(38)
<223> N = T, G, C (6% each); A (82%)

<220>
<221> misc_feature
<222> (39)..(39)
<223> N = A, T, G (1% each); C (97%)

<220>
<221> misc_feature
<222> (40)..(40)
<223> N = T, G, C (6% each); A (82%)

<220>
<221> misc_feature
<222> (41)..(41)
<223> N = A, T, C (6% each); G (82%)

<220>
<221> misc_feature
<222> (42)..(42)
<223> N = A, G, C (6% each); T (82%)

<220>
<221> misc_feature
<222> (43)..(44)
<223> N = T, G, C (6% each); A (82%)

<220>
<221> misc_feature
<222> (45)..(45)
<223> N = A, T, G, C (25% each)

<220>
<221> misc_feature
<222> (46)..(48)
<223> N = A, T, C (6% each); G (82%)

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<400> 78  
 agctatgctg gtctccatt tnnnnnnnnnn nnnnnnnnnnn nnnnnnnngt taaaacagaa 60  
 ctaac 65

<210> 79  
 <211> 36  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Synthetic Oligonucleotide

<400> 79  
 atccagtggg gtctcaaagtg ggaaaagtac aattag 36

<210> 80  
 <211> 63  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Synthetic Oligonucleotide

<220>  
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 <222> (23)..(23)  
 <223> N = A, G, C (6% each); T (82%)

<220>  
 <221> misc\_feature  
 <222> (24)..(26)  
 <223> N = A, T, G (6% each); C (82%)

<220>  
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 <222> (27)..(27)  
 <223> N = A, G, C (6% each); T (82%)

<220>  
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 <222> (28)..(28)  
 <223> N = A, T, G (6% each); C (82%)

<220>  
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 <222> (29)..(30)  
 <223> N = T, G, C (6% each); A (82%)

<220>  
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 <222> (31)..(31)  
 <223> N = A, G, C (6% each); T (82%)

<220>  
 <221> misc\_feature  
 <222> (32)..(32)  
 <223> N = T, G, C (6% each); A (82%)

<220>  
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 <222> (33)..(33)  
 <223> N = A, T, G (6% each); C (82%)

<220>  
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 <222> (34)..(34)  
 <223> N = A, T, G (6% each); C (82%)

<220>  
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 <222> (35)..(35)  
 <223> N = A, T, G (6% each); C (82%)

<220>  
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 <223> N = A, G, C (6% each); T (82%)

<220>  
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 <222> (37)..(37)  
 <223> N = A, T, G (6% each); C (82%)

<220>  
 <221> misc\_feature  
 <222> (38)..(38)  
 <223> N = A, T, G (6% each); C (82%)

<220>  
 <221> misc\_feature  
 <222> (39)..(39)  
 <223> N = T, G, C (6% each); A (82%)

<220>  
 <221> misc\_feature  
 <222> (40)..(40)  
 <223> N = A, T, C (6% each); G (82%)

<220>  
 <221> misc\_feature  
 <222> (41)..(41)  
 <223> N = A, C (8% each); T (1%); G (83%)

<220>  
 <221> misc\_feature  
 <222> (42)..(42)  
 <223> N = T, G, C (6% each); A (82%)

<220>  
 <221> misc\_feature

<222> (43)..(43)  
<223> N = A, T, C (6% each); G (82%)

<220>  
<221> misc\_feature  
<222> (44)..(44)  
<223> N = A, G, C (6% each); T (82%)

<220>  
<221> misc\_feature  
<222> (45)..(45)  
<223> N = T, G, C (6% each); A (82%)

<220>  
<221> misc\_feature  
<222> (46)..(46)  
<223> N = A, T, G (1% each); C (97%)

<400> 80  
catttttacg gatccaattt tttnnnnnnnnn nnnnnnnnnnn nnnnnnnggac caactttttt 60  
  
gag 63

<210> 81  
<211> 62  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic Oligonucleotide

<220>  
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<222> (28)..(28)  
<223> N = A, G, C (6% each); T (82%)

<220>  
<221> misc\_feature  
<222> (29)..(29)  
<223> N = T, G, C (6% each); A (82%)

<220>  
<221> misc\_feature  
<222> (30)..(30)  
<223> N = A, T, G (1% each); C (97%)

<220>  
<221> misc\_feature  
<222> (31)..(33)  
<223> N = A, G, C (6% each); T (82%)

<220>  
<221> misc\_feature  
<222> (34)..(35)  
<223> N = A, T, C (6% each); G (82%)

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<220>
<221> misc_feature
<222> (36)..(36)
<223> N = A, T, G, C (25% each)

<220>
<221> misc_feature
<222> (37)..(37)
<223> N = A (82%); T (2%); G, C (8% each)

<220>
<221> misc_feature
<222> (38)..(39)
<223> N = T, G, C (6% each); A (82%)

<220>
<221> misc_feature
<222> (40)..(40)
<223> N = A, T, C (6% each); G (82%)

<220>
<221> misc_feature
<222> (41)..(41)
<223> N = T, G, C (6% each); A (82%)

<220>
<221> misc_feature
<222> (42)..(42)
<223> N = A, G, C (6% each); T (82%)

<400> 81
gaatttcata cgcgtcttca acctggtnnn nnnnnnnnnn nntctttcaa ttattggtct 60

gg 62

<210> 82
<211> 73
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Oligonucleotide

<220>
<221> misc_feature
<222> (41)..(41)
<223> N = A, G, C (6% each); T (82%)

<220>
<221> misc_feature
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<223> N = A (0%); T,C (9% each); G (82%)

<220>

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<221> misc\_feature  
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 <223> N = A, T, G (6% each); C (82%)

<220>  
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 <222> (46)..(46)  
 <223> N = A, T, G, C (25% each)

<220>  
 <221> misc\_feature  
 <222> (47)..(48)  
 <223> N = T, G, C (6% each); A (82%)

<220>  
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 <223> N = A, G, C (6% each); T (82%)

<220>  
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 <222> (50)..(51)  
 <223> N = A, T, C (6% each); G (82%)

<220>  
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 <222> (52)..(52)  
 <223> N = A, G, C (6% each); T (82%)

<220>  
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 <223> N = T, G, C (6% each); A (82%)

<220>  
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 <222> (55)..(55)  
 <223> N = A, T, C (6% each); G (82%)

<400> 82  
 aaaagtttat cgaactatag ctaatacaga cgtagcggct nnnnnnnnnn nnnnngtata 60  
 tttagtggtt acg 73

<210> 83  
 <211> 20  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Synthetic Oligonucleotide

<400> 83  
 ggagttccat ttgctggggc 20

<210> 84  
 <211> 17  
 <212> DNA  
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 <223> Synthetic Oligonucleotide  
  
 <400> 84  
 atctccataa aatgggg 17

<210> 85  
 <211> 32  
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 <400> 85  
 gcgaagtaaa agaagccaag gtcgaataag gg 32

<210> 86  
 <211> 43  
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 <223> Synthetic Oligonucleotide  
  
 <400> 86  
 cctttaagtt tgcgaaatcc acacagccaa ggtcgaataa ggg 43

<210> 87  
 <211> 35  
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 <223> Synthetic Oligonucleotide  
  
 <400> 87  
 cccattttat gatgttcggt tataacccaaa agggg 35

<210> 88  
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 <220>  
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 <400> 88

ggccaagtga agacccatgg aaggc 25

<210> 89  
<211> 22  
<212> DNA  
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<220>  
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<400> 89  
gcagtttccg gattcgaagt gc 22

<210> 90  
<211> 17  
<212> DNA  
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<220>  
<223> Synthetic Oligonucleotide

<400> 90  
ccgctacgtc tgtatta 17

<210> 91  
<211> 17  
<212> DNA  
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<220>  
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<400> 91  
ataatggaag cacctga 17

<210> 92  
<211> 60  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic Oligonucleotide

<220>  
<221> misc\_feature  
<222> (22)..(22)  
<223> N = T, G, C (6% each); A (82%)

<220>  
<221> misc\_feature  
<222> (23)..(23)  
<223> N = A, G, C (6% each); T (82%)



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<220>
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<222> (24)..(24)
<223> N = A, T, C (6% each); G (82%)

<220>
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<222> (25)..(25)
<223> N = A, T, G (6% each); C (82%)

<220>
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<222> (26)..(26)
<223> N = T, G, C (6% each); A (82%)

<220>
<221> misc_feature
<222> (27)..(28)
<223> N = A, T, C (6% each); G (82%)

<220>
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<222> (29)..(29)
<223> N = T, G, C (6% each); A (82%)

<220>
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<222> (30)..(31)
<223> N = A, T, G (6% each); C (82%)

<220>
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<222> (32)..(32)
<223> N = A, T, C (6% each); G (82%)

<220>
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<222> (33)..(33)
<223> N = A, G, C (6% each); T (82%)

<220>
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<222> (34)..(34)
<223> N = A, T, G (6% each); C (82%)

<220>
<221> misc_feature
<222> (35)..(35)
<223> N = A, T, C (6% each); G (82%)

<220>
<221> misc_feature
<222> (36)..(36)
<223> N = A, G, C (6% each); T (82%)

<220>

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<221> misc\_feature  
 <222> (37)..(38)  
 <223> N = A, T, C (6% each); G (82%)

<220>  
 <221> misc\_feature  
 <222> (39)..(39)  
 <223> N = A, T, G, C (25% each)

<400> 92  
 agctatgctg gtctcttctt annnnnnnnn nnnnnnnnna caattccatt ttttacttgg 60

<210> 93  
 <211> 40  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Synthetic Oligonucleotide

<400> 93  
 atccagttgg gtctctaaga aacaaaccgc gtaattaagc 40

<210> 94  
 <211> 20  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Synthetic Oligonucleotide

<400> 94  
 cctcaagggt tataacatcc 20

<210> 95  
 <211> 55  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Synthetic Oligonucleotide

<220>  
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 <222> (19)..(19)  
 <223> N = A, T, C (6% each); G (82%)

<220>  
 <221> misc\_feature  
 <222> (20)..(20)  
 <223> N = T, G, C (6% each); A (82%)

<220>

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<221> misc_feature
<222> (21)..(21)
<223> N = A, G, C (6% each); T (82%)

<220>
<221> misc_feature
<222> (22)..(23)
<223> N = A, T, C (6% each); G (82%)

<220>
<221> misc_feature
<222> (24)..(24)
<223> N = A, T, G, C (25% each)

<220>
<221> misc_feature
<222> (25)..(25)
<223> N = A, G (8% each); T (2%); C (82%)

<220>
<221> misc_feature
<222> (26)..(27)
<223> N = T, G, C (6% each); A (82%)

<220>
<221> misc_feature
<222> (28)..(28)
<223> N = A (82%); T (2%); G,C (8% each)

<220>
<221> misc_feature
<222> (29)..(30)
<223> N = T, G, C (6% each); A (82%)

<220>
<221> misc_feature
<222> (31)..(31)
<223> N = A, T, C (6% each); G (82%)

<220>
<221> misc_feature
<222> (32)..(32)
<223> N = A, G, C (6% each); T (82%)

<220>
<221> misc_feature
<222> (33)..(33)
<223> N = A, T, G, C (25% each)

<220>
<221> misc_feature
<222> (34)..(34)
<223> N = A, G, C (6% each); T (82%)

<220>
<221> misc_feature
<222> (35)..(35)

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<223> N = T, G, C (6% each); A (82%)

<220>

<221> misc\_feature

<222> (36)..(36)

<223> N = A, G, C (1% each); T (97%)

<400> 95

gtacaaaagc taagctttnn nnnnnnnnnn nnnnnncgaa ctatagctaa tacag 55

<210> 96

<211> 7

<212> PRT

<213> Bacillus thuringiensis

<400> 96

Ser Lys Arg Ser Gln Asp Arg  
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<210> 97

<211> 1959

<212> DNA

<213> Bacillus thuringiensis

<220>

<221> CDS

<222> (1)..(1956)

<400> 97

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1 5 10 15

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat 96  
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn  
20 25 30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg 144  
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met  
35 40 45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat 192  
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp  
50 55 60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta 240  
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val  
65 70 75 80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt 288  
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu  
85 90 95

aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca	336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala	
100 105 110	
caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt	384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser	
115 120 125	
aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat	432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr	
130 135 140	
gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt	480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser	
145 150 155 160	
aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt	528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser	
165 170 175	
cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg	576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val	
180 185 190	
ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta	624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu	
195 200 205	
tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa	672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu	
210 215 220	
gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac	720
Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr	
225 230 235 240	
act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga	768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg	
245 250 255	
ggg tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa	816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu	
260 265 270	
atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat	864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp	
275 280 285	
att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att	912
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile	
290 295 300	
ttt acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca	960
Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro	
305 310 315 320	
act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat	1008

Thr	Phe	Leu	Ser	Ile	Glu	Asn	Ser	Ile	Arg	Lys	Pro	His	Leu	Phe	Asp		
				325					330					335			
tat	tta	cag	ggg	att	gaa	ttt	cat	acg	cgt	ctt	caa	cct	ggt	tac	ttt	1056	
Tyr	Leu	Gln	Gly	Ile	Glu	Phe	His	Thr	Arg	Leu	Gln	Pro	Gly	Tyr	Phe		
			340					345					350				
ggg	aaa	gat	tct	ttc	aat	tat	tgg	tct	ggt	aat	tat	gta	gaa	act	aga	1104	
Gly	Lys	Asp	Ser	Phe	Asn	Tyr	Trp	Ser	Gly	Asn	Tyr	Val	Glu	Thr	Arg		
			355				360					365					
cct	agt	ata	gga	tct	agt	aag	aca	att	act	tcc	cca	ttt	tat	gga	gat	1152	
Pro	Ser	Ile	Gly	Ser	Ser	Lys	Thr	Ile	Thr	Ser	Pro	Phe	Tyr	Gly	Asp		
			370				375				380						
aaa	tct	act	gaa	cct	gta	caa	aag	cta	agc	ttt	gat	gga	caa	aaa	gtt	1200	
Lys	Ser	Thr	Glu	Pro	Val	Gln	Lys	Leu	Ser	Phe	Asp	Gly	Gln	Lys	Val		
					390					395					400		
tat	cga	act	ata	gct	aat	aca	gac	gta	gcg	gct	tgg	ccg	aat	ggt	aag	1248	
Tyr	Arg	Thr	Ile	Ala	Asn	Thr	Asp	Val	Ala	Ala	Trp	Pro	Asn	Gly	Lys		
				405					410					415			
gta	tat	tta	ggt	gtt	acg	aaa	gtt	gat	ttt	agt	caa	tat	gat	gat	caa	1296	
Val	Tyr	Leu	Gly	Val	Thr	Lys	Val	Asp	Phe	Ser	Gln	Tyr	Asp	Asp	Gln		
			420					425					430				
aaa	aat	gaa	act	agt	aca	caa	aca	tat	gat	tca	aaa	aga	aac	aat	ggc	1344	
Lys	Asn	Glu	Thr	Ser	Thr	Gln	Thr	Tyr	Asp	Ser	Lys	Arg	Asn	Asn	Gly		
			435				440					445					
cat	gta	agt	gca	cag	gat	tct	att	gac	caa	tta	ccg	cca	gaa	aca	aca	1392	
His	Val	Ser	Ala	Gln	Asp	Ser	Ile	Asp	Gln	Leu	Pro	Pro	Glu	Thr	Thr		
			450				455				460						
gat	gaa	cca	ctt	gaa	aaa	gca	tat	agt	cat	cag	ctt	aat	tac	gcg	gaa	1440	
Asp	Glu	Pro	Leu	Glu	Lys	Ala	Tyr	Ser	His	Gln	Leu	Asn	Tyr	Ala	Glu		
					470					475					480		
tgt	ttc	tta	atg	cag	gac	cgt	cgt	gga	aca	att	cca	ttt	ttt	act	tgg	1488	
Cys	Phe	Leu	Met	Gln	Asp	Arg	Arg	Gly	Thr	Ile	Pro	Phe	Phe	Thr	Trp		
				485					490					495			
aca	cat	aga	agt	gta	gac	ttt	ttt	aat	aca	att	gat	gct	gaa	aag	att	1536	
Thr	His	Arg	Ser	Val	Asp	Phe	Phe	Asn	Thr	Ile	Asp	Ala	Glu	Lys	Ile		
			500					505					510				
act	caa	ctt	cca	gta	gtg	aaa	gca	tat	gcc	ttg	tct	tca	ggt	gct	tcc	1584	
Thr	Gln	Leu	Pro	Val	Val	Lys	Ala	Tyr	Ala	Leu	Ser	Ser	Gly	Ala	Ser		
			515				520					525					
att	att	gaa	ggt	cca	gga	ttc	aca	gga	gga	aat	tta	cta	ttc	cta	aaa	1632	
Ile	Ile	Glu	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Asn	Leu	Leu	Phe	Leu	Lys		
			530				535				540						
gaa	tct	agt	aat	tca	att	gct	aaa	ttt	aaa	gtt	aca	tta	aat	tca	gca	1680	
Glu	Ser	Ser	Asn	Ser	Ile	Ala	Lys	Phe	Lys	Val	Thr	Leu	Asn	Ser	Ala		

545	550	555	560	
gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act				1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr	565	570	575	
aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc				1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile	580	585	590	
tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca				1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr	595	600	605	
ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag				1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys	610	615	620	
aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc				1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile	625	630	635	640
tat ata gat aag ata gaa ttt atc cca gta caa ttg taa				1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu	645	650		

<210> 98  
 <211> 652  
 <212> PRT  
 <213> Bacillus thuringiensis

<400> 98

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Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met	35	40	45	
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp	50	55	60	
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val	65	70	75	80
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu	85	90	95	
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala	100	105	110	
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser	115	120	125	

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr  
 130 135 140  
 Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser  
 145 150 155 160  
 Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser  
 165 170 175  
 His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val  
 180 185 190  
 Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu  
 195 200 205  
 Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu  
 210 215 220  
 Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr  
 225 230 235 240  
 Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg  
 245 250 255  
 Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu  
 260 265 270  
 Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp  
 275 280 285  
 Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile  
 290 295 300  
 Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro  
 305 310 315 320  
 Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp  
 325 330 335  
 Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe  
 340 345 350  
 Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg  
 355 360 365  
 Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp  
 370 375 380  
 Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val  
 385 390 395 400  
 Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys  
 405 410 415  
 Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln  
 420 425 430



Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly  
 435 440 445  
 His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr  
 450 455 460  
 Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu  
 465 470 475 480  
 Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp  
 485 490 495  
 Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile  
 500 505 510  
 Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser  
 515 520 525  
 Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys  
 530 535 540  
 Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala  
 545 550 555 560  
 Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr  
 565 570 575  
 Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile  
 580 585 590  
 Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr  
 595 600 605  
 Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys  
 610 615 620  
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 625 630 635 640  
 Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu  
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<211> 2000

<212> DNA

<213> Artificial sequence

<220>

<223> Recombinant delta endotoxin

<400> 99

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gaggaactta actacaagga gtttctccgg atgaccgaag atagctccac tgaggttctc 180

gataactcta cagtgaagga cgctgttgga actggcatta gcgttggtggg acagattctt	240
ggagtgggttg gtgttccatt cgctggagct ttgaccagct tctaccagtc ctttctcaac	300
accatctggc cttcagatgc tgatccctgg aaggctttca tggcccaagt ggaagtcttg	360
atcgataaga agatcgaaga gtatgccaaag tctaaagcct tggctgagtt gcaaggtttg	420
cagaacaact tcgaggatta cgtcaacgca ctcaacagct ggaagaaaac tcccttgagt	480
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gaatgggggtt actccagtga agatgttgcc gagttctacc gtaggcagct caagttgact	720
caacagtaca cagaccactg cgtcaactgg tacaacgttg ggctcaatgg tcttagagga	780
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acagagctga ccagagacat cttcacccgat cccatcttcc tacttacgac cctgcagaaa	960
tacggtccaa cttttctctc cattgagaac agcatcagga agcctcacct cttcgactat	1020
ctgcaaggca ttgagtttca caccaggttg caacctggtt acttcggtaa ggattccttc	1080
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taccttgag ttactaaagt ggacttctcc caatacgacg atcagaagaa cgagacatct	1320
actcaaacct acgatagtaa gaggaacaat ggccatgttt ccgcacaaga ctccattgac	1380
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cacaggtctg tcgacttctt taacactatc gacgctgaga agattacca acttcccgtg	1560
gtcaaggctt atgccttgtc cagcggagct tccatcattg aaggccagg cttcaccggt	1620
ggcaacttgc tcttcttaaa ggagtccagc aactccatcg ccaagttcaa agtgacactt	1680
aactcagcag ccttgctcca acgttacagg gttcgtatca gatacgcaag cactaccaat	1740
cttcgcctct ttgtccagaa cagcaacaat gatttccttg tcatctacat caacaagact	1800
atgaacaaag acgatgacct cacctaccaa acattcgatc ttgccactac caatagtaac	1860

atgggattct ctggtgacaa gaacgagctg atcatagggtg ctgagagctt tgtctctaata 1920  
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<210> 100  
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 <212> PRT  
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<220>  
 <223> Recombinant delta endotoxin

<400> 100

Met	Ala	Asn	Pro	Asn	Asn	Arg	Ser	Glu	His	Asp	Thr	Ile	Lys	Val	Thr	1	5	10	15
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Asn	Pro	Asn	Ser	Thr	Leu	Glu	Glu	Leu	Asn	Tyr	Lys	Glu	Phe	Leu	Arg	35	40	45	
Met	Thr	Glu	Asp	Ser	Ser	Thr	Glu	Val	Leu	Asp	Asn	Ser	Thr	Val	Lys	50	55	60	
Asp	Ala	Val	Gly	Thr	Gly	Ile	Ser	Val	Val	Gly	Gln	Ile	Leu	Gly	Val	65	70	75	80
Val	Gly	Val	Pro	Phe	Ala	Gly	Ala	Leu	Thr	Ser	Phe	Tyr	Gln	Ser	Phe	85	90	95	
Leu	Asn	Thr	Ile	Trp	Pro	Ser	Asp	Ala	Asp	Pro	Trp	Lys	Ala	Phe	Met	100	105	110	
Ala	Gln	Val	Glu	Val	Leu	Ile	Asp	Lys	Lys	Ile	Glu	Glu	Tyr	Ala	Lys	115	120	125	
Ser	Lys	Ala	Leu	Ala	Glu	Leu	Gln	Gly	Leu	Gln	Asn	Asn	Phe	Glu	Asp	130	135	140	
Tyr	Val	Asn	Ala	Leu	Asn	Ser	Trp	Lys	Lys	Thr	Pro	Leu	Ser	Leu	Arg	145	150	155	160
Ser	Lys	Arg	Ser	Gln	Asp	Arg	Ile	Arg	Glu	Leu	Phe	Ser	Gln	Ala	Glu	165	170	175	
Ser	His	Phe	Arg	Asn	Ser	Met	Pro	Ser	Phe	Ala	Val	Ser	Lys	Phe	Glu	180	185	190	
Val	Leu	Phe	Leu	Pro	Thr	Tyr	Ala	Gln	Ala	Ala	Asn	Thr	His	Leu	Leu	195	200	205	
Leu	Leu	Lys	Asp	Ala	Gln	Val	Phe	Gly	Glu	Glu	Trp	Gly	Tyr	Ser	Ser				

210	215	220
Glu Asp Val Ala Glu Phe Tyr Arg Arg Gln Leu Lys Leu Thr Gln Gln 225 230 235 240		
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Arg Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg 260 265 270		
Glu Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr 275 280 285		
Asp Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp 290 295 300		
Ile Phe Thr Asp Pro Ile Phe Leu Leu Thr Thr Leu Gln Lys Tyr Gly 305 310 315 320		
Pro Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe 325 330 335		
Asp Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr 340 345 350		
Phe Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr 355 360 365		
Arg Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly 370 375 380		
Asp Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys 385 390 395 400		
Val Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly 405 410 415		
Lys Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp 420 425 430		
Gln Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn 435 440 445		
Gly His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr 450 455 460		
Thr Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala 465 470 475 480		
Glu Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr 485 490 495		
Trp Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys 500 505 510		
Ile Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala		

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Ser Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu		
530	535	540
Lys Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser		
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Ala Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr		
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Thr Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val		
	580	585
Ile Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln		
	595	600
Thr Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp		
	610	620
Lys Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys		
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Ile Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu		
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 aatcacaacc agtaccatt ggctgacaat cctaacagta ctcttgagga acttaactac 180  
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 gaagagtatg ccaagtctaa agccttggct gagttgcaag gtttgcagaa caacttcgag 480  
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 tcccaggacc gtattcgtga acttttcagc caagccgaat cccacttcag aaactccatg 600  
 cctagctttg ccgtttctaa gttcgaggtg ctcttcttgc caacatacgc acaagctgcc 660

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gacctcacct acaacacatt cgatcttgcc actaccaata gtaacatggg attctctggt 1920
gacaagaacg agctgatcat aggtgctgag agctttgtct ctaatgagaa gatttacata 1980
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tatcaagctt 2050

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<210> 102
<211> 2280
<212> DNA
<213> Bacillus thuringiensis

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<400> 102
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ttataatggt caatagtttt atgggaaggc attttatcag gtagaaagt atgtattatg	180
ataagaatgg gaggaagaaa aatgaatcca aacaatcgaa gtgaacatga tacgataaag	240
gttacaccta acagtgaatt gcaaaactaac cataatcaat atccttttagc tgacaatcca	300
aattcaacac tagaagaatt aaattataaa gaatttttaa gaatgactga agacagttct	360
acggaagtgc tagacaactc tacagtaaaa gatgcagttg ggacaggaat ttctgttgta	420
gggcagatth taggtgttgt aggagttcca tttgctgggg cactcacttc attttatcaa	480
tcattttctta acactatatg gccaaagtga gctgacccat ggaaggcttt tatggcacia	540
gttgaagtac tgatagataa gaaaatagag gagtatgcta aaagtaaagc tcttgacagag	600
ttacagggtc ttcaaaataa tttcgaagat tatgttaatg cgttaaattc ctggaagaaa	660
acacctttta gtttgcaag taaaagaagc caagatcgaa taagggaact tttttctcaa	720
gcagaaagtc attttcgtaa ttccatgccg tcatttgacg tttccaaatt cgaagtgtctg	780
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gtttttggag aagaatgggg atattcttca gaagatgttg ctgaatttta tcatagacia	900
ttaaaactta cacaacaata cactgacat tgtgttaatt ggtataatgt tggattaaat	960
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gattctattg accaattacc gccagaaaca acagatgaac cacttgaaaa agcatatagt	1620
catcagctta attacgcgga atgtttctta atgcaggacc gtcgtggaac aattccattt	1680
tttacttgga cacatagaag tgtagacttt ttaatacaa ttgatgctga aaagattact	1740

caacttccag tagtgaaagc atatgccttg tcttcaggtg cttccattat tgaaggtcca	1800
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attaataaaa ctatgaataa agatgatgat ttaacatatc aaacatttga tctcgcaact	2040
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ggagatttta aaatgttggg tgatggtcaa aatgaaagaa taggaaggtg aattttgatg	2220
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<210> 103  
 <211> 32  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Synthetic Oligonucleotide

<400> 103	
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<210> 104  
 <211> 42  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Synthetic Oligonucleotide

<400> 104	
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<210> 105  
 <211> 28  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Synthetic Oligonucleotide

<400> 105	
gacctcacct accaaacatt cgatcttg	28

<210> 106  
 <211> 25



<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic Oligonucleotide

<400> 106  
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<210> 107  
<211> 1959  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Recombinant delta endotoxin

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aattataaag aattttttaag aatgactgaa gacagttcta cggaagtgct agacaactct 180  
acagtaaaag atgcagttgg gacaggaatt tctgtttagtag ggcagatttt aggtgttgta 240  
ggagttccat ttgctggggc actcacttca ttttatcaat catttcttaa cactatatgg 300  
ccaagtgatg ctgacccatg gaaggctttt atggcacaag ttgaagtact gatagataag 360  
aaaatagagg agtatgctaa aagtaaagct cttgcagagt tacagggtct tcaaaataat 420  
ttcgaagatt atgttaatgc gttaaattcc tggaagaaaa cacctttaag tttgcgaagt 480  
aaaagaagcc aaggtcgaat aagggaactt ttttctcaag cagaaagtca ttttcgtaat 540  
tccatgccgt catttgcagt ttccaaattc gaagtgtgtt ttctaccaac atatgcacaa 600  
gctgcaaata cacatttatt gctattaaaa gatgctcaag tttttggaga agaatgggga 660  
tattcttcag aagatgttgc tgaattctat cgtagacaat taaaacttac acaacaatac 720  
actgaccatt gtgttaattg gtataatgtt ggattaaatg gttaagagg ttcaacttat 780  
gatgcatggg tcaaatttaa ccgttttcgc agagaaatga ctttaactgt attagatcta 840  
attgtacttt tcccatttta tgatattcgg ttataactcaa aaggggttaa aacagaacta 900  
acaagagaca tttttacgga tccaattttt ttacttacta cgcttcagaa gtacggacca 960  
acttttttga gtatagaaaa ctctattcga aaacctcatt tatttgatta tttacagggg 1020  
attgaatttc atacgcgtct tcaacctggt tactttggga aagattcttt caattattgg 1080  
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 gttacgaaag ttgatttttag tcaatatgat gatcaaaaaa atgaaactag tacacaaaca 1320  
 tatgattcaa aaagaaacaa tggccatgta agtgcacagg attctattga ccaattaccg 1380  
 ccagaaacaa cagatgaacc acttgaaaaa gcatatagtc atcagcttaa ttacgcggaa 1440  
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 gtagactttt ttaatacaat tgatgctgaa aagattactc aacttccagt agtgaaagca 1560  
 tatgccttgt cttcaggtgc ttccattatt gaaggtccag gattcacagg aggaaattta 1620  
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 tttgtgcaaa attcaaacaa tgattttctt gtcacttaca ttaataaaac tatgaataaa 1800  
 gatgatgatt taacatatca aacatttgat ctcgcaacta ctaattctaa tatgggggttc 1860  
 tcgggtgata agaatgaact tataatagga gcagaatctt tcgtttctaa tgaaaaaatc 1920  
 tatatagata agatagaatt tatcccagta caattgtaa 1959

<210> 108  
 <211> 652  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Recombinant delta endotoxin

<400> 108

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			20					25					30		
Pro	Asn	Ser	Thr	Leu	Glu	Glu	Leu	Asn	Tyr	Lys	Glu	Phe	Leu	Arg	Met
			35				40					45			
Thr	Glu	Asp	Ser	Ser	Thr	Glu	Val	Leu	Asp	Asn	Ser	Thr	Val	Lys	Asp
	50					55					60				
Ala	Val	Gly	Thr	Gly	Ile	Ser	Val	Val	Gly	Gln	Ile	Leu	Gly	Val	Val
65					70					75				80	
Gly	Val	Pro	Phe	Ala	Gly	Ala	Leu	Thr	Ser	Phe	Tyr	Gln	Ser	Phe	Leu
				85					90					95	

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala  
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 Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser  
 115 120 125  
 Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr  
 130 135 140  
 Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser  
 145 150 155 160  
 Lys Arg Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser  
 165 170 175  
 His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val  
 180 185 190  
 Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu  
 195 200 205  
 Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu  
 210 215 220  
 Asp Val Ala Glu Phe Tyr Arg Arg Gln Leu Lys Leu Thr Gln Gln Tyr  
 225 230 235 240  
 Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg  
 245 250 255  
 Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu  
 260 265 270  
 Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp  
 275 280 285  
 Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile  
 290 295 300  
 Phe Thr Asp Pro Ile Phe Leu Leu Thr Thr Leu Gln Lys Tyr Gly Pro  
 305 310 315 320  
 Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp  
 325 330 335  
 Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe  
 340 345 350  
 Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg  
 355 360 365  
 Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp  
 370 375 380  
 Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val  
 385 390 395 400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys  
 405 410 415  
 Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln  
 420 425 430  
 Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly  
 435 440 445  
 His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr  
 450 455 460  
 Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu  
 465 470 475 480  
 Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp  
 485 490 495  
 Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile  
 500 505 510  
 Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser  
 515 520 525  
 Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys  
 530 535 540  
 Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala  
 545 550 555 560  
 Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr  
 565 570 575  
 Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile  
 580 585 590  
 Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr  
 595 600 605  
 Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys  
 610 615 620  
 Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile  
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 Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu  
 645 650

<210> 109

<211> 649

<212> PRT

<213> Artificial sequence

<220>

<223> Recombinant delta endotoxin

<400> 109

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20 25 30  
Pro Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Arg Thr Thr  
35 40 45  
Asp Asn Asn Val Glu Ala Leu Asp Ser Ser Thr Thr Lys Asp Ala Ile  
50 55 60  
Gln Lys Gly Ile Ser Ile Ile Gly Asp Leu Leu Gly Val Val Gly Phe  
65 70 75 80  
Pro Tyr Gly Gly Ala Leu Val Ser Phe Tyr Thr Asn Leu Leu Asn Thr  
85 90 95  
Ile Trp Pro Gly Glu Asp Pro Leu Lys Ala Phe Met Gln Gln Val Glu  
100 105 110  
Ala Leu Ile Asp Gln Lys Ile Ala Asp Tyr Ala Lys Asp Lys Ala Thr  
115 120 125  
Ala Glu Leu Gln Gly Leu Lys Asn Val Phe Lys Asp Tyr Val Ser Ala  
130 135 140  
Leu Asp Ser Trp Asp Lys Thr Pro Leu Thr Leu Arg Asp Gly Arg Ser  
145 150 155 160  
Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser His Phe Arg  
165 170 175  
Arg Ser Met Pro Ser Phe Ala Val Ser Gly Tyr Glu Val Leu Phe Leu  
180 185 190  
Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu Leu Lys Asp  
195 200 205  
Ala Gln Ile Tyr Gly Thr Asp Trp Gly Tyr Ser Thr Asp Asp Leu Asn  
210 215 220  
Glu Phe His Thr Lys Gln Lys Asp Leu Thr Ile Glu Tyr Thr Asn His  
225 230 235 240  
Cys Ala Lys Trp Tyr Lys Ala Gly Leu Asp Lys Leu Arg Gly Ser Thr  
245 250 255  
Tyr Glu Glu Trp Val Lys Phe Asn Arg Tyr Arg Arg Glu Met Thr Leu  
260 265 270  
Thr Val Leu Asp Leu Ile Thr Leu Phe Pro Leu Tyr Asp Val Arg Thr  
275 280 285  
Tyr Thr Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Val Leu Thr Asp

290	295	300															
Pro	Ile	Val	Ala	Val	Asn	Asn	Met	Asn	Gly	Tyr	Gly	Thr	Thr	Phe	Ser		
305					310					315					320		
Asn	Ile	Glu	Asn	Tyr	Ile	Arg	Lys	Pro	His	Leu	Phe	Asp	Tyr	Leu	His		
				325					330					335			
Ala	Ile	Gln	Phe	His	Ser	Arg	Leu	Gln	Pro	Gly	Tyr	Phe	Gly	Thr	Asp		
			340					345					350				
Ser	Phe	Asn	Tyr	Trp	Ser	Gly	Asn	Tyr	Val	Ser	Thr	Arg	Ser	Ser	Ile		
		355					360					365					
Gly	Ser	Asp	Glu	Ile	Ile	Arg	Ser	Pro	Phe	Tyr	Gly	Asn	Lys	Ser	Thr		
	370					375					380						
Leu	Asp	Val	Gln	Asn	Leu	Glu	Phe	Asn	Gly	Glu	Lys	Val	Phe	Arg	Ala		
385					390					395					400		
Val	Ala	Asn	Gly	Asn	Leu	Ala	Val	Trp	Pro	Val	Gly	Thr	Gly	Gly	Thr		
			405					410						415			
Lys	Ile	His	Ser	Gly	Val	Thr	Lys	Val	Gln	Phe	Ser	Gln	Tyr	Asn	Asp		
		420					425						430				
Arg	Lys	Asp	Glu	Val	Arg	Thr	Gln	Thr	Tyr	Asp	Ser	Lys	Arg	Asn	Val		
		435					440					445					
Gly	Gly	Ile	Val	Phe	Asp	Ser	Ile	Asp	Gln	Leu	Pro	Pro	Ile	Thr	Thr		
	450					455				460							
Asp	Glu	Ser	Leu	Glu	Lys	Ala	Tyr	Ser	His	Gln	Leu	Asn	Tyr	Val	Arg		
465					470					475					480		
Cys	Phe	Leu	Leu	Gln	Gly	Gly	Arg	Gly	Ile	Ile	Pro	Val	Phe	Thr	Trp		
		485					490							495			
Thr	His	Lys	Ser	Val	Asp	Phe	Tyr	Asn	Thr	Leu	Asp	Ser	Glu	Lys	Ile		
		500					505						510				
Thr	Gln	Ile	Pro	Phe	Val	Lys	Ala	Phe	Ile	Leu	Val	Asn	Ser	Thr	Ser		
		515				520				525							
Val	Val	Ala	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Asp	Ile	Ile	Lys	Cys	Thr		
	530				535					540							
Asn	Gly	Ser	Gly	Leu	Thr	Leu	Tyr	Val	Thr	Pro	Ala	Pro	Asp	Leu	Thr		
545					550					555					560		
Tyr	Ser	Lys	Thr	Tyr	Lys	Ile	Arg	Ile	Arg	Tyr	Ala	Ser	Thr	Ser	Gln		
		565				570				575							
Val	Arg	Phe	Gly	Ile	Asp	Leu	Gly	Ser	Tyr	Thr	His	Ser	Ile	Ser	Tyr		
		580				585				590							
Phe	Asp	Lys	Thr	Met	Asp	Lys	Gly	Asn	Thr	Leu	Thr	Tyr	Asn	Ser	Phe		

595		600		605
Asn Leu Ser Ser Val Ser Arg Pro Ile Glu Ile Ser Gly Gly Asn Lys				
610		615		620
Ile Gly Val Ser Val Gly Gly Ile Gly Ser Gly Asp Glu Val Tyr Ile				
625		630		635
				640
Asp Lys Ile Glu Phe Ile Pro Met Asp				
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<210> 110  
 <211> 652  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Recombinant delta endotoxin

<400> 110

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro				
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				15
Asn Ser Glu Leu Pro Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn				
	20		25	30
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met				
	35		40	45
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp				
	50		55	60
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val				
65		70		75
				80
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu				
	85		90	95
Asp Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala				
	100		105	110
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser				
	115		120	125
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr				
	130		135	140
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser				
145		150		155
				160
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser				
	165		170	175
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val				
	180		185	190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu  
 195 200 205  
 Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu  
 210 215 220  
 Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr  
 225 230 235 240  
 Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg  
 245 250 255  
 Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu  
 260 265 270  
 Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp  
 275 280 285  
 Val Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile  
 290 295 300  
 Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro  
 305 310 315 320  
 Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp  
 325 330 335  
 Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Ser  
 340 345 350  
 Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg  
 355 360 365  
 Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp  
 370 375 380  
 Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val  
 385 390 395 400  
 Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys  
 405 410 415  
 Ile Tyr Phe Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln  
 420 425 430  
 Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly  
 435 440 445  
 His Val Gly Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr  
 450 455 460  
 Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu  
 465 470 475 480  
 Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp  
 485 490 495



Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile  
 500 505 510  
 Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser  
 515 520 525  
 Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys  
 530 535 540  
 Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala  
 545 550 555 560  
 Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr  
 565 570 575  
 Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Ile Val Ile  
 580 585 590  
 Tyr Ile Asn Lys Thr Met Asn Ile Asp Asp Asp Leu Thr Tyr Gln Thr  
 595 600 605  
 Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Thr  
 610 615 620  
 Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile  
 625 630 635 640  
 Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu  
 645 650

<210> 111  
 <211> 652  
 <212> PRT  
 <213> Artificial sequence  
 <220>  
 <223> Recombinant delta endotoxin

<400> 111

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro  
 1 5 10 15  
 Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn  
 20 25 30  
 Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met  
 35 40 45  
 Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp  
 50 55 60  
 Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val  
 65 70 75 80  
 Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu  
 85 90 95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala  
 100 105 110  
 Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser  
 115 120 125  
 Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr  
 130 135 140  
 Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser  
 145 150 155 160  
 Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser  
 165 170 175  
 His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val  
 180 185 190  
 Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu  
 195 200 205  
 Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu  
 210 215 220  
 Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr  
 225 230 235 240  
 Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg  
 245 250 255  
 Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu  
 260 265 270  
 Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp  
 275 280 285  
 Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile  
 290 295 300  
 Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro  
 305 310 315 320  
 Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp  
 325 330 335  
 Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe  
 340 345 350  
 Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg  
 355 360 365  
 Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp  
 370 375 380  
 Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val  
 385 390 395 400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys  
 405 410 415  
 Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln  
 420 425 430  
 Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly  
 435 440 445  
 His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr  
 450 455 460  
 Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu  
 465 470 475 480  
 Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp  
 485 490 495  
 Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile  
 500 505 510  
 Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser  
 515 520 525  
 Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys  
 530 535 540  
 Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala  
 545 550 555 560  
 Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr  
 565 570 575  
 Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile  
 580 585 590  
 Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr  
 595 600 605  
 Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys  
 610 615 620  
 Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile  
 625 630 635 640  
 Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu  
 645 650

<210> 112

<211> 659

<212> PRT

<213> Artificial sequence

<220>

<223> Recombinant delta endotoxin

<400> 112

Met	Ile	Arg	Met	Gly	Gly	Arg	Lys	Met	Asn	Pro	Asn	Asn	Arg	Ser	Glu	
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Tyr	Asp	Thr	Ile	Lys	Val	Thr	Pro	Asn	Ser	Glu	Leu	Pro	Thr	Asn	His	
			20					25					30			
Asn	Gln	Tyr	Pro	Leu	Ala	Asp	Asn	Pro	Asn	Ser	Thr	Leu	Glu	Glu	Leu	
		35					40					45				
Asn	Tyr	Lys	Glu	Phe	Leu	Arg	Met	Thr	Ala	Asp	Asn	Ser	Thr	Glu	Val	
	50					55					60					
Leu	Asp	Ser	Ser	Thr	Val	Lys	Asp	Ala	Val	Gly	Thr	Gly	Ile	Ser	Val	
65					70					75					80	
Val	Gly	Gln	Ile	Leu	Gly	Val	Val	Gly	Val	Pro	Phe	Ala	Gly	Ala	Leu	
				85					90					95		
Thr	Ser	Phe	Tyr	Gln	Ser	Phe	Leu	Asn	Ala	Ile	Trp	Pro	Ser	Asp	Ala	
			100					105					110			
Asp	Pro	Trp	Lys	Ala	Phe	Met	Ala	Gln	Val	Glu	Val	Leu	Ile	Asp	Lys	
		115					120					125				
Lys	Ile	Glu	Glu	Tyr	Ala	Lys	Ser	Lys	Ala	Leu	Ala	Glu	Leu	Gln	Gly	
	130					135					140					
Leu	Gln	Asn	Asn	Phe	Glu	Asp	Tyr	Val	Asn	Ala	Leu	Asp	Ser	Trp	Lys	
145					150					155					160	
Lys	Ala	Pro	Val	Asn	Leu	Arg	Ser	Arg	Arg	Ser	Gln	Asp	Arg	Ile	Arg	
				165					170					175		
Glu	Leu	Phe	Ser	Gln	Ala	Glu	Ser	His	Phe	Arg	Asn	Ser	Met	Pro	Ser	
			180					185					190			
Phe	Ala	Val	Ser	Lys	Phe	Glu	Val	Leu	Phe	Leu	Pro	Thr	Tyr	Ala	Gln	
		195					200					205				
Ala	Ala	Asn	Thr	His	Leu	Leu	Leu	Leu	Lys	Asp	Ala	Gln	Val	Phe	Gly	
	210					215					220					
Glu	Glu	Trp	Gly	Tyr	Ser	Ser	Glu	Asp	Ile	Ala	Glu	Phe	Tyr	Gln	Arg	
225					230					235				240		
Gln	Leu	Lys	Leu	Thr	Gln	Gln	Tyr	Thr	Asp	His	Cys	Val	Asn	Trp	Tyr	
				245					250					255		
Asn	Val	Gly	Leu	Asn	Ser	Leu	Arg	Gly	Ser	Thr	Tyr	Asp	Ala	Trp	Val	
			260					265					270			
Lys	Phe	Asn	Arg	Phe	Arg	Arg	Glu	Met	Thr	Leu	Thr	Val	Leu	Asp	Leu	
		275					280					285				

Ile Val Leu Phe Pro Phe Tyr Asp Val Arg Leu Tyr Ser Lys Gly Val  
 290 295 300  
 Lys Thr Glu Leu Thr Arg Asp Ile Phe Thr Asp Pro Ile Phe Thr Leu  
 305 310 315 320  
 Asn Ala Leu Gln Glu Tyr Gly Pro Thr Phe Ser Ser Ile Glu Asn Ser  
 325 330 335  
 Ile Arg Lys Pro His Leu Phe Asp Tyr Leu Arg Gly Ile Glu Phe His  
 340 345 350  
 Thr Arg Leu Arg Pro Gly Tyr Ser Gly Lys Asp Ser Phe Asn Tyr Trp  
 355 360 365  
 Ser Gly Asn Tyr Val Glu Thr Arg Pro Ser Ile Gly Ser Asn Asp Thr  
 370 375 380  
 Ile Thr Ser Pro Phe Tyr Gly Asp Lys Ser Ile Glu Pro Ile Gln Lys  
 385 390 395 400  
 Leu Ser Phe Asp Gly Gln Lys Val Tyr Arg Thr Ile Ala Asn Thr Asp  
 405 410 415  
 Ile Ala Ala Phe Pro Asp Gly Lys Ile Tyr Phe Gly Val Thr Lys Val  
 420 425 430  
 Asp Phe Ser Gln Tyr Asp Asp Gln Lys Asn Glu Thr Ser Thr Gln Thr  
 435 440 445  
 Tyr Asp Ser Lys Arg Tyr Asn Gly Tyr Leu Gly Ala Gln Asp Ser Ile  
 450 455 460  
 Asp Gln Leu Pro Pro Glu Thr Thr Asp Glu Pro Leu Glu Lys Ala Tyr  
 465 470 475 480  
 Ser His Gln Leu Asn Tyr Ala Glu Cys Phe Leu Met Gln Asp Arg Arg  
 485 490 495  
 Gly Thr Ile Pro Phe Phe Thr Trp Thr His Arg Ser Val Asp Phe Phe  
 500 505 510  
 Asn Thr Ile Asp Ala Glu Lys Ile Thr Gln Leu Pro Val Val Lys Ala  
 515 520 525  
 Tyr Ala Leu Ser Ser Gly Ala Ser Ile Ile Glu Gly Pro Gly Phe Thr  
 530 535 540  
 Gly Gly Asn Leu Leu Phe Leu Lys Glu Ser Ser Asn Ser Ile Ala Lys  
 545 550 555 560  
 Phe Lys Val Thr Leu Asn Ser Ala Ala Leu Leu Gln Arg Tyr Arg Val  
 565 570 575  
 Arg Ile Arg Tyr Ala Ser Thr Thr Asn Leu Arg Leu Phe Val Gln Asn  
 580 585 590

Ser Asn Asn Asp Phe Leu Val Ile Tyr Ile Asn Lys Thr Met Asn Ile  
595 600 605

Asp Gly Asp Leu Thr Tyr Gln Thr Phe Asp Phe Ala Thr Ser Asn Ser  
610 615 620

Asn Met Gly Phe Ser Gly Asp Thr Asn Asp Phe Ile Ile Gly Ala Glu  
625 630 635 640

Ser Phe Val Ser Asn Glu Lys Ile Tyr Ile Asp Lys Ile Glu Phe Ile  
645 650 655

Pro Val Gln

<210> 113  
<211> 652  
<212> PRT  
<213> Artificial sequence  
<220>  
<223> Recombinant delta endotoxin  
<400> 113

Met Ile Arg Lys Gly Gly Arg Lys Met Asn Pro Asn Asn Arg Ser Glu  
1 5 10 15

His Asp Thr Ile Lys Thr Thr Glu Asn Asn Glu Val Pro Thr Asn His  
20 25 30

Val Gln Tyr Pro Leu Ala Glu Thr Pro Asn Pro Thr Leu Glu Asp Leu  
35 40 45

Asn Tyr Lys Glu Phe Leu Arg Met Thr Ala Asp Asn Asn Thr Glu Ala  
50 55 60

Leu Asp Ser Ser Thr Thr Lys Asp Val Ile Gln Lys Gly Ile Ser Val  
65 70 75 80

Val Gly Asp Leu Leu Gly Val Val Gly Phe Pro Phe Gly Gly Ala Leu  
85 90 95

Val Ser Phe Tyr Thr Asn Phe Leu Asn Thr Ile Trp Pro Ser Glu Asp  
100 105 110

Pro Trp Lys Ala Phe Met Glu Gln Val Glu Ala Leu Met Asp Gln Lys  
115 120 125

Ile Ala Asp Tyr Ala Lys Asn Lys Ala Leu Ala Glu Leu Gln Gly Leu  
130 135 140

Gln Asn Asn Val Glu Asp Tyr Val Ser Ala Leu Ser Ser Trp Gln Lys  
145 150 155 160

Asn Pro Val Ser Ser Arg Asn Pro His Ser Gln Gly Arg Ile Arg Glu  
165 170 175

Leu Phe Ser Gln Ala Glu Ser His Phe Arg Asn Ser Met Pro Ser Phe  
180 185 190

Ala Ile Ser Gly Tyr Glu Val Leu Phe Leu Thr Thr Tyr Ala Gln Ala  
 195 200 205  
 Ala Asn Thr His Leu Phe Leu Leu Lys Asp Ala Gln Ile Tyr Gly Glu  
 210 215 220  
 Glu Trp Gly Tyr Glu Lys Glu Asp Ile Ala Glu Phe Tyr Lys Arg Gln  
 225 230 235 240  
 Leu Lys Leu Thr Gln Glu Tyr Thr Asp His Cys Val Lys Trp Tyr Asn  
 245 250 255  
 Val Gly Leu Asp Lys Leu Arg Gly Ser Ser Tyr Glu Ser Trp Val Asn  
 260 265 270  
 Phe Asn Arg Tyr Arg Arg Glu Met Thr Leu Thr Val Leu Asp Leu Ile  
 275 280 285  
 Ala Leu Phe Pro Leu Tyr Asp Val Arg Leu Tyr Pro Lys Glu Val Lys  
 290 295 300  
 Thr Glu Leu Thr Arg Asp Val Leu Thr Asp Pro Ile Val Gly Val Asn  
 305 310 315 320  
 Asn Leu Arg Gly Tyr Gly Thr Thr Phe Ser Asn Ile Glu Asn Tyr Ile  
 325 330 335  
 Arg Lys Pro His Leu Phe Asp Tyr Leu His Arg Ile Gln Phe His Thr  
 340 345 350  
 Arg Phe Gln Pro Gly Tyr Tyr Gly Asn Asp Ser Phe Asn Tyr Trp Ser  
 355 360 365  
 Gly Asn Tyr Val Ser Thr Arg Pro Ser Ile Gly Ser Asn Asp Ile Ile  
 370 375 380  
 Thr Ser Pro Phe Tyr Gly Asn Lys Ser Ser Glu Pro Val Gln Asn Leu  
 385 390 395 400  
 Glu Phe Asn Gly Glu Lys Val Tyr Arg Ala Val Ala Asn Thr Asn Leu  
 405 410 415  
 Ala Val Trp Pro Ser Ala Val Tyr Ser Gly Val Thr Lys Val Glu Phe  
 420 425 430  
 Ser Gln Tyr Asn Asp Gln Thr Asp Glu Ala Ser Thr Gln Thr Tyr Asp  
 435 440 445  
 Ser Lys Arg Asn Val Gly Ala Val Ser Trp Asp Ser Ile Asp Gln Leu  
 450 455 460  
 Pro Pro Glu Thr Thr Asp Glu Pro Leu Glu Lys Gly Tyr Ser His Gln  
 465 470 475 480  
 Leu Asn Tyr Val Met Cys Phe Leu Met Gln Gly Ser Arg Gly Thr Ile  
 485 490 495

Pro Val Leu Thr Trp Thr His Lys Ser Val Asp Phe Phe Asn Met Ile  
 500 505 510  
 Asp Ser Lys Lys Ile Thr Gln Leu Pro Leu Val Lys Ala Tyr Lys Leu  
 515 520 525  
 Gln Ser Gly Ala Ser Val Val Ala Gly Pro Arg Phe Thr Gly Gly Asp  
 530 535 540  
 Ile Ile Gln Cys Thr Glu Asn Gly Ser Ala Ala Thr Ile Tyr Val Thr  
 545 550 555 560  
 Pro Asp Val Ser Tyr Ser Gln Lys Tyr Arg Ala Arg Ile His Tyr Ala  
 565 570 575  
 Ser Thr Ser Gln Ile Thr Phe Thr Leu Ser Leu Asp Gly Ala Pro Phe  
 580 585 590  
 Asn Gln Tyr Tyr Phe Asp Lys Thr Ile Asn Lys Gly Asp Thr Leu Thr  
 595 600 605  
 Tyr Asn Ser Phe Asn Leu Ala Ser Phe Ser Thr Pro Phe Glu Leu Ser  
 610 615 620  
 Gly Asn Asn Leu Gln Ile Gly Val Thr Gly Leu Ser Ala Gly Asp Lys  
 625 630 635 640  
 Val Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Asn  
 645 650